


```
Db 62 VLDKTKAKKVDIVAHSMGGANTLYIYKLDGGDKIENVVIGGANGLVSSRA,PGTDPNQ 121
Qy 121 KILYTSYSSADMIVMNYLSKLDGAKNQVHGIGHGILLMNSQVNSLIKEGLNGGLNTN 180
Db 122 KILYTSYSSADLIIVNSLSRLGARNVLIHGVIHGLTSSQVKGYKEGLNGGQNTN 181

RESULT 2
Q8VU78 PRELIMINARY; PRT; 215 AA.
AC 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Lipase.
OS Bacillus sp. B26.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=117494;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B26;
RA Kim M.H., Kim H.K., Oh T.K., Lee J.K.;
RT "Cloning and sequencing of a lipase gene from Bacillus sp. B26.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF232707; AAL36938.1; -.
DR GO; GO:0003824; P: catalytic activity; IEA.
DR GO; GO:0016298; P: lipase activity; IEA.
DR GO; GO:0016042; P: lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Ser_eatrs.
DR Pfam; PF01674; Lipase 2; 1.
SQ SEQUENCE 215 AA; 22959 MW; 460397D7026A789B CRC64;

Query Match 78.1%; Score 733; DB 2; Length 215;
Best Local Similarity 77.2%; Pred. No. 3.8e-50;
Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;

Qy 1 EHNPMVVMHGGGASFNAGIKSYLVSGWGRKLYAVFDWKTGTNNYNGPVLSPFKK 60
Db 36 EHNPMVVMHGGGASFNAGIKSYLVSGWQDQNLFAIDFDKGTNNLNGPRLSRVKD 95

Qy 61 VLDKTKAKKVDIVAHSMGGANTLYIYKLDGGKVENVVTIGGTRSTTSKALPGTDPNQ 120
Db 96 VLAKTGAKKVDIVAHSMGGANTLYIYKLDGGDKIENVVIGGANGLVSLRALPGTDPNQ 155

Qy 121 KILYTSYSSADMIVMNYLSKLDGAKNQVHGIGHGILLMNSQVNSLIKEGLNGGLNTN 180
Db 156 KILYTSYSSADLIIVNSLSRLGARNVLIHGVIHGLTSSQVKGYKEGLNGGQNTN 215

RESULT 3
P94444 PRELIMINARY; PRT; 210 AA.
AC P94444;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Extracellular esterase precursor (EC 3.1.1.1) (Yfip).
GN LIPA OR LIPE.
OS Bacillus sp. BP-6, and
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=187867; 1423;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Bacillus sp. BP-6; STRAIN=BP-6;
RA Ruiz C., Pastor J., Diaz P.;
RT "Identification and cloning of Bacillus megaterium and Bacillus sp.
RT BP-6 esterases. Comparison with Bacillus subtilis and Bacillus pumilus
RT lipases.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
[2]
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RP SEQUENCE FROM N.A.
RC SPECIES=B.subtilis; STRAIN=AC327;
RX MEDLINE=97128783; PubMed=8973323;
RA Yamamoto H., Uchiyama S., Sekiguchi J.;
RT "The Bacillus subtilis chromosome region near 78 degrees contains the
RT a lipase.";
RL Gene 181:147-151 (1996).
RN [3]

RP SEQUENCE FROM N.A.
RC SPECIES=B.subtilis; STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maubert C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Fujita P., Purnelle B., Rapoport G., Ray M., Sadale Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256 (1997).
RN [4]

RP SEQUENCE FROM N.A.
RC SPECIES=B.subtilis; STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ30985; CAD24006.1; -.
DR EMBL; D78508; BAA11406.1; -.
DR EMBL; Z99108; CAB12664.1; -.
DR PIR; C69652; C69652.
DR GO; GO:0016787; F: hydrolase activity; IEA.
DR GO; GO:0016298; F: lipase activity; IEA.
DR GO; GO:0004759; F: serine esterase activity; IEA.
DR GO; GO:0016042; P: lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Ser_eatrs.
DR Pfam; PF01674; Lipase 2; 1.
KW Hydrolase; Signal; Complete proteome.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 210 EXTRACELLULAR ESTERASE.
SQ SEQUENCE 210 AA; 22363 MW; 4359843F882C690A CRC64;

Query Match 76.0%; Score 714; DB 16; Length 210;
Best Local Similarity 74.3%; Pred. No. 1.2e-48;
Matches 133; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

Qy 2 HNPVVMHGGGASFNAGIKSYLVSGWGRKLYAVFDWKTGTNNYNGPVLSPFKV 61
Db 32 HNPVLMVHGTSASYNFPAIKNYLISQGWQSKLYAIDFYDKTGNLNGPQLASYDVR 91

Qy 62 LDSTGAKKVDIVAHSMGGANTLYIYKLDGGKVENVVTIGGTRSTTSKALPGTDPNQ 121
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Db 92 LKETGAKKVDIVAHSMGGANTLYIKYLGGNKIQNVVTLGGANGLVSTALPGTDPNQK 151
QY 122 ILVTSYSSADMVNMVYSLKDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 152 ILVTSYSLNDQIVNSLSRQAGNIQYIGHIGLLNSQVNGYIKGGLNGGLNTN 210

RESULT 4
Q8RUP5 PRELIMINARY; PRT; 210 AA.
AC Q8RUP5;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Extracellular esterase precursor (EC 3.1.1.1).
GN LipA.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC3985;
RA Ruiz C., Pastor J., Diaz P.;
RT "Identification and cloning of Bacillus megaterium and Bacillus sp.
RT BP-6 esterases. Comparison with Bacillus subtilis and Bacillus pumilus
RT lipases.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ430831; CAD23620.1; -.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0016298; F:lipase activity; IEA.
DR GO: GO:0004759; F:serine esterase activity; IEA.
DR GO: GO:0016042; F:lipid catabolism; IEA.
DR InterPro: IPR002918; Ser_estrs.
DR Pfam: PF01674; Lipase_2; 1.
DR Signal; Hydrolase.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 210 EXTRACELLULAR ESTERASE.
SQ SEQUENCE 210 AA; 22411 MW; 9408989882C6918 CRC64;

Query Match 74.8%; Score 702; DB 2; Length 210;
Best Local Similarity 73.2%; Pred. No. 1e-47;
Matches 131; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 2 HNPVVMVHGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDKTGTNNYNGPVLRSFVKV 61
Db 32 HNPVLMVHGIGGASFNFAIKNYLSQGSQSNKLYAIDFYDKTGNLNLNGPQLASVYDRV 91
QY 62 LDETGAKKVDIVAHSMGGANTLYIKYKLDGNGKVENVVTLLGGTNRSTTSKALPGTDPNQK 121
Db 92 LKETGAKKVDIVAHSMGGANTLYIKYLGGNKIQNVVTLGGANGLVSTALPGTDPNQK 151
QY 122 ILVTSYSSADMVNMVYSLKDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 152 ILVTSYSLNDQIVNSLSRQAGNIQYIGHIGLLNSQVNGYIKGGLNGGLNTN 210

RESULT 5
Q83VDO PRELIMINARY; PRT; 201 AA.
AC Q83VDO;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE PLA depolymerase.
GN PLA.
OS Paenibacillus amylolyticus.
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1451;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TB-13;

Query Match 74.8%; Score 702; DB 2; Length 210;
Best Local Similarity 73.2%; Pred. No. 1e-47;
Matches 131; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 2 HNPVVMVHGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDKTGTNNYNGPVLRSFVKV 61
Db 32 HNPVLMVHGIGGASFNFAIKNYLSQGSQSNKLYAIDFYDKTGNLNLNGPQLASVYDRV 91
QY 62 LDETGAKKVDIVAHSMGGANTLYIKYKLDGNGKVENVVTLLGGTNRSTTSKALPGTDPNQK 121
Db 92 LKETGAKKVDIVAHSMGGANTLYIKYLGGNKIQNVVTLGGANGLVSTALPGTDPNQK 151
QY 122 ILVTSYSSADMVNMVYSLKDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
Db 152 ILVTSYSLNDQIVNSLSRQAGNIQYIGHIGLLNSQVNGYIKGGLNGGLNTN 210
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RA MEDLINE=22617435; PubMed=12732514;
RA Akutsu-Shigeno Y., Teeraphatpornchai T., Teamtisong K., Nomura N.,
RA Uchiyama H., Nakahara T., Nakajima-Kambe T.;
RT "Cloning and Sequencing of a Poly(DL-Lactic Acid) Depolymerase Gene
RT from Paenibacillus amylolyticus Strain TB-13 and Its Functional
RT Expression in Escherichia coli.";
RL Appl. Environ. Microbiol. 69:2498-2504 (2003).
DR EMBL: AB093482; BAC67195.1; -.
DR GO: GO:0003824; F:catalytic activity; IEA.
DR GO: GO:0016298; F:lipase activity; IEA.
DR GO: GO:0016042; P:lipid catabolism; IEA.
DR InterPro: IPR002918; Lipase_2.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF01674; Lipase_2; 1.
SQ SEQUENCE 201 AA; 21661 MW; 4771183D38B7FBE1 CRC64;

Query Match 45.9%; Score 431; DB 2; Length 201;
Best Local Similarity 52.9%; Pred. No. 2.5e-26;
Matches 91; Conservative 24; Mismatches 51; Indels 6; Gaps 1;

QY 1 EHNVPVVMVHGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDKTGTNNYNGPVLRSFVKV 60
Db 34 ERTPTIVFVHGLTGTSCNPFALIERYLRCGEGSSDSELFADLPFSKAGNOLLNSAALSRFVDD 93
QY 61 VLDETGAKKVDIVAHSMGGANTLYIKYKLDGNGKVENVVTLLGGTNRSTTSKALPGTDPNQ 120
Db 94 VLRTGSHKVDIVAHSMGGANSLYILNRGGIDKVDKLTILGGANRLTTSRDPG----- 148
QY 121 KILVTSYSSADMVNMVYSLKDGAKNVQIHGVGHIGLLMNSQVNSLIKEGL 172
Db 149 -IRVTSYSTSTIVSPALSRDGNANNISVNLVTHIGLLYNSRVNLIKAAAL 199

RESULT 6
Q826T6 PRELIMINARY; PRT; 228 AA.
AC Q826T6;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Putative lipase.
GN SAV7089.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531 (2003).
DR EMBL: AF050549; BAC74800.1; -.
DR GO: GO:0003824; F:catalytic activity; IEA.
DR GO: GO:0016298; F:lipase activity; IEA.
DR GO: GO:0016042; P:lipid catabolism; IEA.
DR InterPro: IPR002918; Lipase_2.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF01674; Lipase_2; 1.
DR
```

KW Complete proteome. 228 AA; 24450 MW; C736C01EFF0F9DA9 CRC64;
SQ SEQUENCE 228 AA; 24450 MW; C736C01EFF0F9DA9 CRC64;

Query Match 21.5%; Score 202; DB 16; Length 228;
Best Local Similarity 29.1%; Pred. No. 3.6e-08;
Matches 52; Conservative 33; Mismatches 66; Indels 28; Gaps 4;

QY 2 HNPVVMVHGIGGASFNAGIKSYLVSOQWGRGKLYAVDFW--DKTGTNYNNGPVLGRFVX 59
DB 35 HDPVIFVHGIGSSASSWDDMTADFEADGYTASEL---DMSYDWSQSNVTTAQLATEVR 91
QY 60 KVLDEGAKVDIVVAHSGGANTLYIKNLGGKNKVENVTLTGTNESTT-----109
DB 92 SVLARTGASKVDLVVHSGMALSARYLKNLGGTGYDVPFVSTAGVNRHGTGVASCKWLYT 151
QY 110 -----SKALPCTDPNQKILYTSIYSSA-DMIVMNYLSKLDGAKNVQIHGVGH 155
DB 152 SCSEMYTGSSFLTSLNSGDETPGGVAVASYNSCDDLLTPTDTSAILSGATNVEGCVSH 210

RESULT 7
Q828V2 PRELIMINARY; PRT; 286 AA.
AC Q828V2;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative secreted lipase.
GN SAV6559.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites."
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis."
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AF005047; BAC74270.1; -
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0016298; F: lipase activity; IEA.
DR GO; GO:0016042; P: lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Ser. esters.
DR Pfam; PF01674; Lipase_2; 1.
KW Complete proteome.
SQ SEQUENCE 286 AA; 30158 MW; 29A8703DD3BF853 CRC64;

Query Match 20.6%; Score 193.5; DB 16; Length 286;
Best Local Similarity 35.1%; Pred. No. 2.3e-07;
Matches 54; Conservative 23; Mismatches 60; Indels 17; Gaps 5;

QY 4 PVTVMHG-IGGASFNAGIKSYLVSOGW-----SRGKLYAVDFWKTGTNYNNGPVLGRF 57
DB 52 PVLVHGTGNSVDNWLGLAPYLEHGGYCVFSLDYGLSGVFFHGLGPDIDKASQLQVF 111
QY 58 VKKVLDEGAKVDIVVAHSGGANTLYIKNLGGKNKVENVTLTGTNRSTSKAL-----113

DB 112 VDKVLTATGATKADLVHSGQGMPPRYLYKFLGAGKKNALVGIAPNNHGTTLGLTNLL 171
QY 114 ---PCTDENQKILYTSIYSSADMIYMN-YLSKLD 143
DB 172 PVFPGA---EDLLSTATPGLADQVVGSAFMAKLN 202

RESULT 8
Q9RSP6 PRELIMINARY; PRT; 237 AA.
AC Q9RSP6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Lipase, putative.
GN DR2078.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eissen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Panphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uitterback T., Zalewski C.,
RA Makareva K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AS003044; AAF11628.1; -
DR PIR; G75316; G75316.
DR TIGR; DR2078; -
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0016298; F: lipase activity; IEA.
DR GO; GO:0016042; P: lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Ser. esters.
DR Pfam; PF01674; Lipase_2; 1.
KW Complete proteome.
SQ SEQUENCE 237 AA; 25308 MW; 1C2BF99210B8AF2E CRC64;

Query Match 20.6%; Score 193; DB 16; Length 237;
Best Local Similarity 29.1%; Pred. No. 1.9e-07;
Matches 55; Conservative 37; Mismatches 75; Indels 22; Gaps 5;

QY 3 NPVTVMHGIGGASFNAGIKSYLVSOQWGRGKLYAVDFWKTGTNYNNGPVLGRFVX 62
DB 46 HPVLVHGFNSDGSINWSPMNRFPKQDGTDAQLFSWSY--DSFKSNVATADLRQKVDAIL 104
QY 63 DETGAKKVDIVVAHSGGANTLYIKNLGGKNKVENVTLTGTNR-----STTS----110
DB 105 AQGAQAQVDIVHSHMGALSSRYLYKLGTAQKAVDAVSLGGPNHGTDFALACSTACIEM 164
QY 111 -----KAL-PCTDENQKILYTSIYSSADMIY-MNYLSKLDGAKNVQIHGVGHGLLN 161
DB 165 RQSSFFIKALNSGDETPGAVRYATWSPDVAIPNSVPLSGATNTKTSCLTHSSLYGD 224
QY 162 SQVNSLIKE 170
DB 225 ATVTQVRD 233

RESULT 9
Q9KY65 PRELIMINARY; PRT; 331 AA.
ID Q9KY65
AC Q9KY65;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative secreted lipase.
SC04799 OR SC63A.10C.
Streptomyces coelicolor.
Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
[1]
SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmid and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
[4]
SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Narraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seger K., Saunders D., Sharp S., Squares R., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939121; CAB92662.1;
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0006298; F:lipase activity; IEA.
DR GO; GO:0016042; F:lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR008262; Lipase AS.
DR Pfam; PF01674; Lipase 2; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Complete proteome.
SQ
SEQUENCE 331 AA; 35137 MW; 3E0E77A687747211 CRC64;

Query Match 19.2%; Score 180.5; DB 16; Length 331;
Best Local Similarity 26.7%; Pred. No. 2.9e-06;
Matches 54; Conservative 41; Mismatches 78; Indels 29; Gaps 6;

QY 4 PYVWHGIGGASFNAGIKSYLVSQWSRGKLYAVDFWDKTGTNYNNGPVLRSFVKVLD 63
DB 115 PVVLLHGFDNRSVFLRLRSITQHG--RQAIESLNSPLTCDIRTAELLGRHIEICE 172
QY 64 ETGAKKVDIVAHSMGGANTLYIKNLGDKGNKVENVVTGGTNRSTTSKAL----- 113
DB 173 RTGSEVVDVHSLGGLIARYVQRLGDLRVTLVTLGTPHTGKVVPLANAHPIVRQM 232
QY 114 -PGT-----DPNQKILYTSIYSSADMIVNVLK--LD----GAKNVIHGHHIG 157
DB 233 RPSAVIEELTRPAPGCRTRFVFSWSDLR--VMDPLETACLDHPDLSVQNVRSVGHIA 291
QY 158 LLNNSQVNSLIKEGLNGGLNT 179
DB 292 LPVHPAVATGIRQALDAGPET 313

Query Match 19.2%; Score 180.5; DB 16; Length 331;
Best Local Similarity 26.7%; Pred. No. 2.9e-06;
Matches 54; Conservative 41; Mismatches 78; Indels 29; Gaps 6;

QY 4 PYVWHGIGGASFNAGIKSYLVSQWSRGKLYAVDFWDKTGTNYNNGPVLRSFVKVLD 63
DB 115 PVVLLHGFDNRSVFLRLRSITQHG--RQAIESLNSPLTCDIRTAELLGRHIEICE 172
QY 64 ETGAKKVDIVAHSMGGANTLYIKNLGDKGNKVENVVTGGTNRSTTSKAL----- 113
DB 173 RTGSEVVDVHSLGGLIARYVQRLGDLRVTLVTLGTPHTGKVVPLANAHPIVRQM 232
QY 114 -PGT-----DPNQKILYTSIYSSADMIVNVLK--LD----GAKNVIHGHHIG 157
DB 233 RPSAVIEELTRPAPGCRTRFVFSWSDLR--VMDPLETACLDHPDLSVQNVRSVGHIA 291
QY 158 LLNNSQVNSLIKEGLNGGLNT 179
DB 292 LPVHPAVATGIRQALDAGPET 313
```

RESULT 10

```
Q82HP7
ID Q82HP7 PRELIMINARY; PRT; 286 AA.
AC Q82HP7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative lipase.
GN SAV3461.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AF005035; BAC71173.1;
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR000379; Ser esters.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Complete proteome.
SQ
SEQUENCE 286 AA; 30720 MW; 1C5CE9B5E212B2DD9 CRC64;
```

Query Match 18.4%; Score 172.5; DB 16; Length 286;
Best Local Similarity 25.2%; Pred. No. 1e-05;
Matches 51; Conservative 41; Mismatches 75; Indels 35; Gaps 5;

```
QY 4 PYVWHGIGGASFNAGIKSYLVSQWSRGKLYAVDFWDKTGTNYNNGPVLRSFVKVLD 63
DB 76 PVVLLHGFDNRSVFLRLRSITQHG--RQAIESLNSPLTCDIRTAELLGRHIEICE 133
QY 64 ETGAKKVDIVAHSMGGANTLYIKNLGDKGNKVENVVTGGTNRSTTSKAL----- 113
DB 134 RTGSEVVDVHSLGGLIARYVQRLGDLRVTLVTLGTPHTGKVVPLANAHPIVRQM 193
QY 114 -PGT-----DPNQKILYTSIYSSADMIVNVLK--LD----GAKNVIHGHHIG 154
DB 194 RPSAVIEELTRPAPGCRTRFVFSWSDLR--VMDPLETACVHPDLMVQNVRSVGG 249
QY 155 HIGLNNQVNSLIKEGLNGGG 176
DB 250 HLALPVHPAVATGIRQALDSEG 271
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RESULT 11

```
Q9S295
ID Q9S295 PRELIMINARY; PRT; 290 AA.
AC Q9S295;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative secreted lipase.
GN SCO1735 OR SC111.24C.
```

OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D., Harris D.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
[4]
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=1200953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)."
RL Nature 417:141-147(2002).
RL EMBL; AL939110; CAB50950.1; -.
DR PIR; T36757; T36757.
DR HSSP; Q05489; ITH.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0016298; F:lipase activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Sex esters.
DR Pfam; PF01674; Lipase_2; 1.
KW Complete proteome.
SQ SEQUENCE 290 AA; 30496 MW; D5GE8508350F7432 CRC64;

Query Match 18.1%; Score 170; DB 16; Length 290;
Best Local Similarity 29.2%; Pred. No. 1.7e-05;
Matches 56; Conservative 28; Mismatches 58; Indels 50; Gaps 8;

QY 4 PVTMVGIGGASF-NPAGTKSVLSQWSRGKLYAVDFDKTGNTN-YNNGPV-----L 54
DB 56 PVLVHGTFGNSVDNWLGLAPYKNGKGYC---VFLSDYGLPGLVFLPGLGPFVKSABL 112
QY 55 SRVKKVLDGTGAKKVDIVAHSMGGANTLYIKNLDGGNKVENVTLGGTNRSTT-----S 110
DB 113 AAHVQKVLATGATETDLVGHSGGMPYLYKFLGGAEEVVALVGIAPSNHGTLSGLT 172
QY 111 KALP-----GTDPNQKILVTSYSSADMVWNYL 139
DB 173 RLPLFPFGAEDLLNEHTPALADQWGSVDLTFLNAGGDTVPGRVYTVLATKYDEVVTYR 232
QY 140 SK-LD--GAKNV 148
DB 233 GQFLDGGFGRNV 244

RESULT 12

Q8RC83
ID Q8RC83 PRELIMINARY; PRT; 403 AA.
AC Q8RC83;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Predicted acetyltransferases and hydrolases with the alpha/beta
DE hydrolase fold.
GN LIPA OR TTE0555.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.,
RT "A complete sequence of T. tengcongensis genome."
RL Genome Res. 12:689-700(2002).
DR EMBL; AB013025; AM23831.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0016298; F:lipase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR002918; Lipase 2.
DR InterPro; IPR000379; Sex esters.
DR Pfam; PF01674; Lipase_2; 1.
KW Transferase; Hydrolase; Complete proteome.
SQ SEQUENCE 403 AA; 45221 MW; DC31D5E86EC2CAC4 CRC64;

Query Match 17.9%; Score 168; DB 16; Length 403;
Best Local Similarity 35.9%; Pred. No. 3.7e-05;
Matches 42; Conservative 16; Mismatches 41; Indels 18; Gaps 3;

QY 4 PVTMVGIGGASF-NPFA-----GIKSVLSQWSRGKLYAVDFDKTGNTNNGPVYL 54
DB 102 PVLVHGTFGNSVDNWLGLAPYKNGKGYC---KVFATFAPHGDNVYIQREIL 158
QY 55 SRVKKVLDGTGAKKVDIVAHSMGGANTLYIKNLDGGNKVENVTLGGTNRSTN 105
DB 159 ADVIQKVKAVTGASKVDIVAHSGKNMSARMYVSVKESWGVDGKDVREYIQLGAPN 215

RESULT 13
P73372
ID P73372 PRELIMINARY; PRT; 202 AA.
AC P73372;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (PMGA).
GN SLL1969.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugiyura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Natuo K., Okumura S.,
RA Simpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
RN [2]
RP SEQUENCE OF 27-202 FROM N.A.
RA Hinara Y., Ikeuchi M.;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:01:57 ; Search time 9.18367 Seconds
(without alignments)
1020.575 Million cell updates/sec

Title: US-09-905-666A-75

Perfect score: 939
Sequence: 1 EHNFFVVMVHGIGGASFNPA.....NSQVNSLIKEGLNGGLNTN 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	884	94.1	212	1 LIP_BACSU	P37957 bacillus su
2	129.5	13.8	358	1 LIP_PSEGL	O05489 pseudomonas
3	118.5	12.6	364	1 LIP_BURCE	P22088 Burkholderia
4	118.5	12.6	364	1 LIP_PSEBS	P25275 pseudomonas
5	114	12.1	312	1 LIP_VIBCH	P15493 vibrio chol
6	103	11.0	737	1 ALYS_ENTFA	P37710 enterococcus
7	96.5	10.3	681	1 LIP_STAAM	Q99QX0 staphylococ
8	95.5	10.2	688	1 LIP_STAEP	Q02510 staphylococ
9	94.5	10.1	293	1 MHPG_ECOLI	P77044 escherichia
10	90	9.6	562	1 VMEI_SCHWA	P46508 schistosoma
11	89.5	9.5	690	1 LIP_STAAR	P10335 staphylococ
12	89.5	9.5	690	1 LIP_STAAR	Q8NYC2 staphylococ
13	88	9.4	431	1 ENO_SHEON	Q8EBR0 shewanella
14	86	9.2	277	1 BPHD_PSES1	P17548 pseudomonas
15	86	9.2	1052	1 RTH32_ACTPL	P55131 actinobacil
16	85.5	9.1	605	1 AOR_PYRPU	Q51739 pyrococcus
17	85	9.1	326	1 TGL2_YEAST	P54857 saccharomyc
18	84.5	9.0	351	1 ADH_CLORE	P25984 clostridium
19	84	8.9	268	1 ESL2_MYCPN	P75311 mycoplasma
20	83.5	8.9	373	1 ACCC_ALCEU	P27747 alcaligenes
21	83.5	8.9	1113	1 MGA2_YEAST	P40578 saccharomyc
22	82.5	8.8	234	1 PUR7_STEAB	Q8E7X2 streptococ
23	81.5	8.7	277	1 LIP_PSEFR	P08658 pseudomonas
24	81	8.6	1754	1 PMPE_CHLTR	O84418 chlamydia t
25	80.5	8.6	415	1 YEGM_ECOLI	P76397 escherichia
26	80.5	8.6	607	1 AOR_PYRAB	Q9V035 pyrococcus
27	80	8.5	313	1 YKL4_YEAST	P28321 saccharomyc
28	79.5	8.5	236	1 PUR7_LACIA	O68830 lactococcus
29	79.5	8.5	245	1 EFGF_CAUCR	Q06171 caulobacter
30	79.5	8.5	286	1 BPHD_BURCE	P47229 Burkholderia
31	79.5	8.5	288	1 Y134_MYCTU	O50599 mycobacteri
32	79.5	8.5	306	1 MIAA_BORBU	O51761 borrelia bu
33	79.5	8.5	331	1 KEAK_DROWE	O18391 drosophila

ALIGNMENTS

RESULT 1

LIP_BACSU
ID LIP_BACSU STANDARD; PRT; 212 AA.
AC P37957; C34644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
GN LIPB OR LIP OR BSU02700.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=92329538; PubMed=1320940;
RA Datois V., Baulard A., Schanck K., Colson C.;
RT "Cloning, nucleotide sequence and expression in Escherichia coli of a
RT lipase gene from Bacillus subtilis 168.";
RL Biochim. Biophys. Acta 1131:253-260(1992).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97419516; PubMed=9274031;
RA Kumano M., Tamakoshi A., Yamane K.;
RT "A 32 kb nucleotide sequence from the region of the lincomycin-
RT resistance gene (22 degrees-25 degrees) of the Bacillus subtilis
RT chromosome and identification of the site of the lin-2 mutation.";
RL Microbiology 143:2775-2782(1997).
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Solotkin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerth I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaeser P., Goffeau A., Golligly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haeche J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Kjaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidis A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mavel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro E., Pujic P., Purnelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivalta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

34 79.5 8.5 514 1 TUBE DROVI
35 79 8.4 362 1 MURC SHEON
36 79 8.4 381 1 SUBN_BACNA
37 79 8.4 431 1 ENO_SALTY
38 79 8.4 485 1 Y045_MYCPN
39 78.5 8.4 326 1 VSO9 ROTPY
40 78.5 8.4 369 1 MRP_ECOLI
41 78.5 8.4 607 1 AOR_PVRHO
42 78.5 8.4 691 1 COMA_NEIGO
43 78.5 8.4 1286 1 AIDA_ECOLI
44 78 8.3 719 1 CLPA_BACTK
45 77.5 8.3 311 1 LIP_PSEAE

Q08171 drosophila
Q8CX35 shewanella
P35835 bacillus su
Q8XGP6 salmonella
P75056 mycoplasma
P17466 porcine rot
P21590 escherichia
O58778 pyrococcus
P51973 neisseria g
Q03155 escherichia
Q45752 bacillus th
P26876 pseudomonas

RA Takeuchi M., Tamakoshi A., Tanaka T., Terpatra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vasarotti A.,
RA Viari A., Wambutt R., Wedler H., Yamane K., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RL Nature 390:249-256(1997).
RL NATURE 390:249-256(1997).
CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC -!- SUBCELLULAR LOCATION: Secreted.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M74010; AAA22574.1; -.
DR EMBL: AB000617; BAA22231.1; -.
DR EMBL: Z99105; CAB12064.1; -.
DR FIR: S23934; S23934.
DR PDB: 116W; 06-JUN-01.
DR PDB: 118P; 19-DEC-02.
DR Subtilisin; BG10679; lipA.
DR InterPro: IPR002918; Lipase_2.
DR InterPro: IPR000379; Ser esters.
DR Pfam: PF01674; Lipase_2; 1.
DR Hydrolase; Lipid degradation; Signal; Complete proteome; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 212
FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CONFLICT 133 133 L -> V (IN REF. 1).
FT SEQUENCE 212 AA; 22791 MW; B8A70E027461188F CRC64;
Query Match 94.1%; Score 884; DB 1; Length 212;
Best Local Similarity 93.9%; Pred.No. 3e-68; 7; Indels 0; Gaps 0;
Matches 169; Conservative 4; Mismatches 7;
QY 1 EHNPNVWVHGIGGASFNFAIGKSYLSQGSQKLYAVDFWKTGTNNYNGPVLGRFVKK 60
DB 33 EHNPNVWVHGIGGASFNFAIGKSYLSQGSQKLYAVDFWKTGTNNYNGPVLGRFVKK 92
QY 61 VLDETGAKYDVIHNSGGANTLYIKNLDGGNKVNVLTGNTSTSKALPGTDNQ 120
DB 93 VLDETGAKYDVIHNSGGANTLYIKNLDGGNKVNVLTGNTSTSKALPGTDNQ 152
QY 121 KILYTSYSSADMVVMYLSKLDGAKNVQIHGVGHICLLMNSQVNSLIKEGLNGGGLNTN 180
DB 153 KILYTSYSSADMVVMYLSKLDGAKNVQIHGVGHICLLMNSQVNSLIKEGLNGGGLNTN 212
RESULT 2
LIP_PSEGL STANDARD; PRT; 358 AA.
AC Q05489;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
GN LIPA.
OS Pseudomonas glumae, and
OS Chromobacterium viscosum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=337, 42739;
[1]
RN SEQUENCE FROM N.A., SEQUENCE OF 40-61, AND MUTAGENESIS.
RP SPECIES=P. Glumae; STRAIN=PG1 / CBS 322.89;
RX MEDLINE=93119130; PubMed=1476423;
RA Frenken L.G.J., Egmond M.R., Batenburg A.M., Bos J.W., Visser C.,

Verrips C.T.;
"Cloning of the Pseudomonas glumae lipase gene and determination of
the active site residues.";
Appl. Environ. Microbiol. 58:3787-3791(1992).
[2]
RN SEQUENCE OF 40-54, AND CHARACTERIZATION.
RP SPECIES=C. viscosum;
RX MEDLINE=95306500; PubMed=7786905;
RA Taipa M.A., Liebeton K., Costa J.V., Cabral J.M.S., Jaeger K.-E.;
"Lipase from Chromobacterium viscosum: biochemical characterization
indicating homology to the lipase from Pseudomonas glumae.";
Biochim. Biophys. Acta 1256:396-402(1995).
[3]
RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RP SPECIES=P. Glumae;
RX MEDLINE=94009622; PubMed=8405390;
RA Noble M.B.M., Cleasby A., Johnson L.N., Egmond M.R., Frenken L.G.J.;
"The crystal structure of triacylglycerol lipase from Pseudomonas
glumae reveals a partially redundant catalytic aspartate.";
FEBS Lett. 331:123-128(1993).
[4]
RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RP SPECIES=C. viscosum; STRAIN=ATCC 6918;
RX MEDLINE=96275656; PubMed=8683577;
RA Lang D., Hofmann B., Haalick L., Hecht H.-J., Spener F., Schmid R.D.,
Schomburg D.;
"Crystal structure of a bacterial lipase from Chromobacterium
viscosum ATCC 6918 refined at 1.6-A resolution.";
J. Mol. Biol. 259:704-717(1996).
CC -!- FUNCTION: HYDROLYSIS OF TRIGLYCERIDES.
CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -!- COFACTOR: requires calcium.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
CC LIPASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X70354; CAA49812.1; -.
DR EMBL: A16323; CAA01279.1; -.
DR EMBL: A32021; CAA02073.1; -.
DR FIR: A48952; A48952.
DR PDB: ITAH; 31-MAY-94.
DR PDB: 1CVL; 01-APR-97.
DR PDB: 1QGE; 06-MAY-99.
DR InterPro: IPR000073; A/b hydrolase.
DR InterPro: IPR008262; Lipase AS.
DR InterPro: IPR000379; Ser esters.
DR Pfam: PF00561; abhydrolase; 1.
DR PROSITE: PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Signal; Calcium; 3D-structure.
FT SIGNAL 1 39
FT CHAIN 40 358
FT ACT_SITE 126 126 CHARGE RELAY SYSTEM.
FT ACT_SITE 302 302 CHARGE RELAY SYSTEM.
FT ACT_SITE 324 324 CHARGE RELAY SYSTEM.
FT DISULFID 229 308
FT MUTAGEN 54 54 H->A: NO LOSS OF ACTIVITY.
FT MUTAGEN 126 126 S->A: COMPLETE LOSS OF ACTIVITY.
FT MUTAGEN 160 160 D->E: NO LOSS OF ACTIVITY.
FT MUTAGEN 160 160 D->A: NO LOSS OF ACTIVITY.
FT MUTAGEN 280 280 D->E: NO LOSS OF ACTIVITY.
FT MUTAGEN 280 280 D->A: COMPLETE LOSS OF ACTIVITY.
FT MUTAGEN 302 302 D->E: NO LOSS OF ACTIVITY.
FT MUTAGEN 302 302 D->A: 75% LOSS OF ACTIVITY.

H->A: COMPLETE LOSS OF ACTIVITY.
A -> W (IN REF. 2).

FT MUTAGEN 324 324
FT CONFLICT 40 40
FT TURN 43 44
FT STRAND 50 53
FT TURN 61 62
FT HELIX 65 67
FT TURN 70 71
FT HELIX 72 78
FT TURN 79 80
FT STRAND 83 86
FT TURN 89 90
FT TURN 97 98
FT HELIX 100 115
FT TURN 116 116
FT STRAND 120 125
FT TURN 126 126
FT HELIX 127 138
FT TURN 140 142
FT STRAND 143 149
FT TURN 153 154
FT HELIX 157 168
FT TURN 170 171
FT TURN 173 174
FT HELIX 176 188
FT TURN 191 193
FT HELIX 196 204
FT TURN 205 206
FT HELIX 208 217
FT TURN 221 222
FT STRAND 223 223
FT TURN 226 228
FT STRAND 231 231
FT STRAND 235 238
FT TURN 239 240
FT STRAND 241 248
FT STRAND 250 250
FT STRAND 253 259
FT TURN 260 261
FT STRAND 262 267
FT TURN 275 275
FT HELIX 276 279
FT HELIX 281 284
FT TURN 295 297
FT STRAND 301 301
FT STRAND 306 306
FT HELIX 307 310
FT STRAND 314 315
FT STRAND 320 320
FT TURN 324 325
FT HELIX 326 328
FT TURN 329 333
FT TURN 337 338
FT HELIX 342 356
FT TURN 357 358
SQ SEQUENCE 358 AA; FE7B5D7A22EC6B4B CRC64;
Query Match 13.8%; Score 129.5; DB 1; Length 358;
Best Local Similarity 34.8%; Pred. No. 0.00081;
Matches 40; Conservative 16; Mismatches 42; Indels 17; Gaps 6;
QY 4 PYVMVHGIGGASFNFA-----GKSYLVSGWSRGLKYAVD---FWDKCTGTYNNNGPV 53
Db 49 PVLIVHGLAGTD-KFANVVDYVWYGQSDLOSHG---AKYVYANVLSGFQSDGPN-GRGEQ 103
QY 54 LSRFVKVLDGTGAKVDIVAHSMGAGNTLYIKNLDGNGKVENVTTLGGTNRST 108
Db 104 LLAIVYKQVLAATGATKVNLIHSGQGLTSRYIA--AVAPQLVASVTITGTPHRGS 156
RESULT 3
LIP BURCE
ID LIP BURCE
AC P22088; STANDARD; PRT; 364 AA.

DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
GN LIPA.
OS Burkholderia cepacia (Pseudomonas cepacia).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_taxid=292;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 45-66.
RC STRAIN=DSM 3959;
RX MEDLINE=91100343; PubMed=1987151;
RA Joergensen S., Skov K.W., Diderichsen B.;
RT "Cloning, sequence, and expression of a lipase gene from Pseudomonas
RT cepacia: lipase production in heterologous hosts requires two
RT Pseudomonas Genes.";
RL J. Bacteriol. 173:559-567(1991).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=97184684; PubMed=9032073;
RA Kim K.K., Song H.K., Shin D.H., Hwang K.Y., Suh S.W.;
RT "The crystal structure of a triacylglycerol lipase from Pseudomonas
RT cepacia reveals a highly open conformation in the absence of a bound
RT inhibitor.";
RL Structure 5:173-185(1997).
RN [3]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=97184685; PubMed=9032074;
RA Schrag J.D., Li Y., Cygler M., Lang D., Burgdorf T., Hecht H.-J.,
RA Schmid R., Schomburg D., Rydel T.J., Oliver J.D., Strickland L.C.,
RA Dunaway C.M., Larsen S.B., Day J., McPherson A.;
RT "The open conformation of a Pseudomonas lipase.";
RL Structure 5:187-202(1997).
CC -I- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -I- COPACTOR: Requires calcium.
CC -I- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
CC LIPASE FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL; M58494; AAA50466.1; -;
DR PDB; 1OIL; 15-MAR-97.
DR PDB; 2LIP; 12-MAR-97.
DR PDB; 3LIP; 16-JUN-97.
DR PDB; 1HQD; 22-AUG-98.
DR PDB; 4LIP; 19-AUG-98.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR000379; Ser. esters.
DR Pfam; PF00561; abhydrolase_1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; lipid degradation; Signal; Calcium; 3D-structure.
FT SIGNAL 1 44
FT CHAIN 45 364 LIPASE.
FT ACT_SITE 131 131 CHARGE RELAY SYSTEM.
FT ACT_SITE 286 286 CHARGE RELAY SYSTEM.
FT ACT_SITE 330 330 CHARGE RELAY SYSTEM.
FT TURN 48 49
FT STRAND 55 58
FT TURN 61 62
FT STRAND 66 67
FT TURN 71 72
FT STRAND 75 76
FT TURN 77 78
FT HELIX 77 83

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FT TURN 84 85
FT TURN 88 90
FT TURN 102 103
FT TURN 105 120
FT TURN 121 121
FT TURN 125 130
FT TURN 131 132
FT TURN 133 143
FT TURN 145 147
FT TURN 148 154
FT TURN 158 159
FT TURN 162 171
FT TURN 172 173
FT TURN 175 176
FT TURN 178 194
FT TURN 196 197
FT TURN 204 210
FT TURN 211 211
FT TURN 213 222
FT TURN 226 227
FT TURN 228 228
FT TURN 231 232
FT TURN 236 236
FT TURN 240 242
FT TURN 247 255
FT TURN 258 264
FT TURN 265 266
FT TURN 267 272
FT TURN 273 274
FT TURN 277 279
FT TURN 281 281
FT TURN 282 285
FT TURN 287 300
FT TURN 301 303
FT TURN 307 307
FT TURN 312 312
FT TURN 313 316
FT TURN 320 326
FT TURN 330 331
FT TURN 332 334
FT TURN 335 339
FT TURN 343 344
FT TURN 348 362
FT TURN 363 364
SQ SEQUENCE 364 AA; 37494 MW; E9CD2DBFB55658E9 CRC64;

Query Match 12.6%; Score 118.5; DB 1; Length 364;
Best Local Similarity 29.9%; Pred. No. 0.0072;
Matches 35; Conservative 19; Mismatches 42; Indels 21; Gaps 6;

QY 4 PVMVHGIGGASFPAGIKSYLVSGW-----SRGKLYAVD---FWDKTGTNYNG 51
Db 54 PIILVHGLSGTD-KYAGVLEY-----WYGIQEDLQONGATVYVANLSGFSQDDGPN-GRG 106
QY 52 PVLRSFVKVLDGTGAKKVDIVAHSMGGANTLYIKNLDDGKNVENVVTLGGTNRST 108
Db 107 EQLLAYVKTVLAATGATKVNLVGHSGQLSRYVA--AVAPDLVASVTITGTPHRGS 161

RESULT 4
LIP_PSES5
ID LIP_PSES5 STANDARD; PRT; 364 AA.
AC P25275;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
GN LIP
OS Pseudomonas sp. (strain KWI-56).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=311;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 45-47.
```

```
RX MEDLINE=92118328; PubMed=1368739;
RA Iizumi T., Nakamura K., Shimada Y., Sugihara A., Tominaga Y.,
RA Fukase T.;
RT "Cloning, nucleotide sequencing, and expression in Escherichia coli
RT of a lipase and its activator genes from Pseudomonas sp. KWI-56.";
RL Agric. Biol. Chem. 55:2349-2357(1991).
CC -|- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -|- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
CC LIPASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D10069; BAA0960.1; -
CC HSP; S77842; AAC60400.1; -
CC HSP; P22088; 3LTP.
CC InterPro; IPR000073; A/b_hydrolase.
CC InterPro; IPR008262; Lipase_AS.
CC InterPro; IPR000379; Ser_estrs.
CC Pfam; PF00561; abhydrolase_1.
CC PROSITE; PS00120; LIPASE_SER; 1.
CC Hydrolase; Lipid degradation; Signal.
KW SIGNAL 1 44
FT CHAIN 45 364 LIPASE.
FT ACT_SITE 131 131 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 286 286 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 330 330 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 364 AA; 37511 MW; F346CB8B2E94E27D CRC64;

Query Match 12.6%; Score 118.5; DB 1; Length 364;
Best Local Similarity 29.9%; Pred. No. 0.0072;
Matches 35; Conservative 18; Mismatches 43; Indels 21; Gaps 6;

QY 4 PVMVHGIGGASFPAGIKSYLVSGW-----SRGKLYAVD---FWDKTGTNYNG 51
Db 54 PIILVHGLSGTD-KYAGVLEY-----WYGIQEDLQONGATVYVANLSGFSQDDGAN-GRG 106
QY 52 PVLRSFVKVLDGTGAKKVDIVAHSMGGANTLYIKNLDDGKNVENVVTLGGTNRST 108
Db 107 EQLLAYVKTVLAATGATKVNLVGHSGQLSRYVA--AVAPDLVASVTITGTPHRGS 161

RESULT 5
LIP_VIBCH
ID LIP_VIBCH STANDARD; PRT; 312 AA.
AC P15493; O07349; Q9KMU7;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lactonizing lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
GN LIPA OR HLXC OR VCA0221.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor O17 / Serotype O1;
RX MEDLINE=90286918; PubMed=2162464;
RA Alm R.A., Manning P.A.;
RT "Characterization of the hlyB gene and its role in the production of
RT the El Tor haemolysin of Vibrio cholerae O1.";
RL Mol. Microbiol. 4:413-425(1990).
RN [2]
RP IDENTIFICATION, AND REVISIONS.
RC STRAIN=El Tor O17 / Serotype O1;
RN [1]
RP Manning P.A.;
```


Best Local Similarity 23.3%; Pred. No. 0.34; Matches 48; Conservative 32; Mismatches 90; Indels 36; Gaps 7;
10 GIGGASNFAGIKS-XLVSQWGRGKL---YAVDFWDTGTNNYNGPVL-----SRPVKK- 60
416 GSGSNNQSGTNTYTVKSGDTLNKIAAQYGVSVANLRSWNGISGDLIFVQKLIIVKKG 475
61 VLDETGAKKVDIVAHSMGGANTLYIKULDGGNKV----- 95
476 ASGNTGSGNNGSNNQSGTNTYTVKSGDTLNKIAAQYGVSVANLRSWNGISGDLIFAG 535
96 ENVVTLGTNRSTTSKALPGTDPNQKILYTSIYSSADMVIMVNYLSKLDGAKNVQIHGVGH 155
536 QKIIVKGTSGTNGSGSNNQSGTNTYTVKSGDTLNKIAAQYGVSVANLRSWNGISGDLIFVQKLIIVKKG 594
156 I-GLMNSQVNSLKEGLNGGLNTN 180
595 IGSGLIFAGQKIIVKGANSGSTNTN 620

RESULT 7
LIP STAMP
ID LIP STAMP STANDARD; PRT; 681 AA.
AC Q990X0;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).
GN LIP OR GEH OR SAV2671 OR SA2463.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=158878, 158879;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshizawa A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsuki K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus".
RL Lancet 357:1225-1240 (2001).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
family.

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EMBL; AF003366; BAB58833.1; --
EMBL; AF003138; BAB43769.1; --
PIR; G90075; G90075.
DR InterPro; IPR005877; Gpos_Y5IRK.
DR InterPro; IPR006262; Lipase_AS.
DR InterPro; IPR006379; Ser_estrs.
DR Pfam; PF04650; Y5IRK_signal; 1.
DR TIGRFAMs; TIGR01168; Y5IRK_signal; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Zymogen; Signal; Complete proteome.
FT SIGNAL 1 35
PROPSP 36 291 BY SIMILARITY.

FT CHAIN 292 681 LIPASE.
FT ACT_SITE 409 409
FT ACT_SITE 640 640
SQ SEQUENCE 681 AA; 76662 MW; FE428D6F3B4B2CB4 CRC64;
Query Match 10.3%; Score 96.5; DB 1; Length 681;
Best Local Similarity 22.2%; Pred. No. 1.1; Mismatches 62; Indels 71; Gaps 10;
Matches 46; Conservative 28; IRODLENGY---KAYEASI-SAFGNSYDRAVELYVYIKGR 370
QY 3 NPVVMVHGIGGASNFAGIKSVLSQWGRGKLXAVDFWDTGTNNYNGPVLRSFVKVL 62
Db 318 NPSVLAHVWGNKN---IRODLENGY---KAYEASI-SAFGNSYDRAVELYVYIKGR 370
QY 63 DETGA-----KKVDIVAHSMGGANTLYIKUL----- 89
Db 371 VDYGAHAAYCHERYGKTYEGYKDWKPKQKHLVGHSMGG-QTIQLELLNGHREE 429
QY 90 -----DGG-----NKNVNVTLGTNRSTTSKALPGTDPNQKILYTSIYSSAD 132
Db 430 IEYQKHGGEISPLFKGNNDNMISITLTGTPHNGTHASDLA---NEALVRQIVFD--- 483
QY 133 MIVMNYLSKLDGAKNVQI-HGVGHIGL 158
Db 484 -----IGKMFQKNKNSRVDFGLAQWGL 504

RESULT 8
LIP STAMP
ID LIP STAMP STANDARD; PRT; 688 AA.
AC Q02510;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).
GN LIP OR GEH OR SE0281.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=1282;
[1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 303-315.
RC STRAIN=9;
RX MEDLINE=93171870; PubMed=8436947;
RA Farrell A.M., Foster T.J., Holland K.T.;
RA "Molecular analysis and expression of the lipase of Staphylococcus
RT epidermidis".
RL J. Gen. Microbiol. 139:267-277 (1993).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228)".
RL Mol. Microbiol. 49:1577-1593 (2003).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
family.

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EMBL; M95577; AAA19729.1; --
EMBL; AE016744; AAC03878.1; --
PIR; A47705; A47705.

DR InterPro; IPR005877; Gpos_Y5IRK.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF04650; Y5IRK signal; 1.
DR TIGRFAMs; TIGR01168; Y5IRK signal; 1.
DR PROSITE; PSC0120; LIPASE SER; 1.
KW Hydrolyase; Lipid degradation; Zymogen; Signal; Complete proteome.
FT SIGNAL 1 35
FT PROPEP 36 302
FT CHAIN 303 688
FT ACT_SITE 418 418
FT ACT_SITE 648 648
FT CONFLICT 96 96
FT CONFLICT 120 120
SQ SEQUENCE 688 AA; 77343 MW; 6C95D33A78AF86F6 CRC64;

Query Match 10.2%; Score 95.5; DB 1; Length 688;
Best Local Similarity 22.7%; Pred. No. 1.4;
Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

QY 3 NPVMVHGIGGASFNPAFGIKSVLSQSGSRGKLYAVDFWDTGTNNNGPVLRSFVKVL 62
DB 327 NESVLTHYGGDKMNI---IRQLENGYEAYEASISAF-----GSNYDRAVELYIYIKGR 379
QY 63 DETGA-----KKVDIVAHSMGGANTLYIYIKM----- 89
DB 380 VDYGAHAAYKGYERYKTYEGYKDWKPGQKIHVLVGHSMGG-QTIROLEELLRHGNEE 438
QY 90 -----DGG--NKVENVVTLLGGTNRSTTSKALPGTDPNPKILYTSYSSAD 132
DB 439 VEYQKHGEISPLYOGGHDNMVSSITLTGTPHNGTHASDLLG---NEAIVRLAYD--- 492

QY 133 MIVMNYLSKLDGAKNQI-HGVGHIGL 158
DB 493 -----VGRMYGNKDSRVDFGLEHWGL 513

RESULT 9
MHPC ECOLI STANDARD; PRT; 293 AA.
AC P77054; P71204; P77205;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase (EC 3.7.1.-).
GN MHPC OR B0349.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RA Kawamukai M.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / CS20;
RA Fernandez A., Garcia J.L., Diaz E.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
[4]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;

RA Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- PATHWAY: 3-hydroxyphenylpropionate degradation.
CC -!- SIMILARITY: STRONG, TO B.CEPACIA AND PSEUDOMONAS BPHD.
CC
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CC
DR EMBL; D86239; BAAL3054.1; -;
DR EMBL; Y05555; CAA70749.1; -;
DR EMBL; A000142; AAC73452.1; ALT_INIT.
DR EMBL; U73857; AAB18073.1; ALT_INIT.
DR MEROPS; S33-UNW; -;
DR EcoGene; EG20275; mhpc.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR003089; AB hydrolase.
DR InterPro; IPR000639; Epox hydrolase.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00561; abhydrolase; 1.
DR PRINTS; PR00111; ABHYDROLASE.
DR PRINTS; PR00412; EPOXYHYDLASE.
KW Automatic hydrocarbons catabolism; Hydrolase; Complete proteome.
FT ACT_SITE 90 90 BY SIMILARITY.
FT CONFLICT 158 158 E -> G (IN REF. 1 AND 2).
SQ SEQUENCE 293 AA; 32585 MW; 4407DF7B90EA0B80 CRC64;

Query Match 10.1%; Score 94.5; DB 1; Length 293;
Best Local Similarity 25.1%; Pred. No. 0.61;
Matches 43; Conservative 36; Mismatches 61; Indels 31; Gaps 9;

QY 5 VMVHGIG-GAS--FNPAGIKSVLSQSGSRGKLYAVDFWDTGTNNNG---PVLRSFV 58
DB 43 VLLHSGPGATGWANFSRNDPLVEAGY-RVLLDCPGHGKSDSVVSSRDLNARIL 101
QY 59 KKVLDGTGAKKVDIVAHSMGGANTLYIYKLDGNGKVENVTLL-GGTRSTTSKALP--- 114
DB 102 KSVVDQLDIKIHLLGNSMGHSHVAF--TLKWPVRVGLVLMGGGTGCGSLFTPMPTG 159
QY 115 -----GTPNQKILY-TSIYSSADMI-----VMVLSKLDGAKN 147
DB 160 IKRLNQLYRQFTIENKLMMDIFVFTSDLTDLAFEARLNMLSRDHLN 210

RESULT 10
YMEI SCHMA STANDARD; PRT; 662 AA.
ID YMEI SCHMA
AC P46508;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE YMEI protein homolog (EC 3.4.24.-).
OS Schistosoma mansoni (Blood fluke).
OC Schistosomatoidea; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Liberian;
RA Menrath M.;
RL Thesis (1994), Heinrich-Heine University / Duesseldorf, Germany.
CC -!- FUNCTION: Putative ATP-dependent protease.
CC -!- COPACATOR: Binds 1 zinc ion (potential).
CC -!- SIMILARITY: Belongs to the AAA ATPase family.
CC -!- SIMILARITY: Belongs to peptidase family M41.
CC
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RA Lancel 359;1819-1827(2002).
 CC -|- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -|- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -|- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
 CC family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF004823; BAB394162.1; -
 DR InterPro; IPR005877; Gops YSIRK.
 DR InterPro; IPR008262; Lipase AS.
 DR InterPro; IPR000379; Ser esters.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Hydrolase; Lipid degradation; Zymogen; Signal; Complete proteome.
 FT SIGNAL
 FT PROPEP 38 295 BY SIMILARITY.
 FT CHAIN 296 690 LIPASE (BY SIMILARITY).
 FT ACT_SITE 412 412 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 645 645 CHARGE RELAY SYSTEM (BY SIMILARITY).
 SQ SEQUENCE 690 AA; 76522 MW; 36FF5E0BB434CCA CRC64;
 Query Match 9.5%; Score 89.5; DB 1; Length 690;
 Best Local Similarity 23.3%; Pred. No. 4.5;
 Matches 47; Conservative 21; Mismatches 55; Indels 79; Gaps 8;
 QY 4 PVMVHGI-----GGASPNFAGIKSVLSQGSRSGLYAVDFWDTGTN 47
 Db 306 PVFVHGFLGLVGDNAPALYNYGNGKFK---VIEELKQGINVHQASVAF---GSN 358
 QY 48 YNNGPVLGRFVKVLDETGA-----KKVDIVAHSMGGANT 82
 Db 359 YDRAVELVYIKGGVDYGAHAARKYGHRYKTYKIMENWBPCKVKVHLVGHSMGGQTI 418
 QY 83 LYVIRNLDGKNVE-----NVVTLGGTNR---STTSKALP-----GTD 117
 Db 419 RLMSEFLRNGNKEEAYKANGGELSPLFTGCHNNWVASITLATPNHGQAADKFGNTE 478
 QY 118 PNQKILYT-----SIYSSADM 133
 Db 479 AVRKIMFALNRMGNKYNSIDL 500
 RESULT 13
 ENO SHEON STANDARD; PRT; 431 AA.
 AC Q8EBR0;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
 DE glycerate hydro-lyase).
 GN ENO OR SO3440.
 OS Shewanella oneidensis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Alteromonadaceae; Shewanella.
 OC NCBI_TaxID=70963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WR-1;
 RA MEDLINE=22597686; PubMed=12368813;
 RX Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
 RA Meyer T., Tsagin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,

RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
 RA Vanatteravan J., Weidman J., Imprim M., Lee K., Berry K., Lee C.,
 RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., C.M.,
 RA Feldblyum T.V., Smith A.O., Venter J.C., Neilson K.H., Fraser C.M.,
 RT Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT Shewanella oneidensis.
 RL Nat. Biotechnol. 20:1118-1123(2002).
 CC -|- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
 CC H(2)O.
 CC -|- COFACTOR: Magnesium is required for catalysis and for stabilizing
 CC the dimer (By similarity).
 CC -|- PATHWAY: Glycolysis
 CC -|- SUBUNIT: Homodimer (By similarity).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -|- SIMILARITY: Belongs to the enolase family.
 CC
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 CC
 CC EMBL; AE015780; AAN56437.1; ALT_INIT.
 DR TIGR; SO3440; -
 DR HAMAP; MF_00318; -; 1.
 DR InterPro; IPR000941; Enolase.
 DR Pfam; PF00113; enolase; 1.
 DR Pfam; PF03952; enolase N; 1.
 DR PRINTS; PR00148; ENOLASE.
 DR PRODOM; PD000902; Enolase; 1.
 DR TIGRFAMs; TIGR01060; eno; 1.
 DR PROSITE; PS00164; ENOLASE; 1.
 KW Lyase; Glycolysis; Magnesium; Complete proteome.
 FT ACT_SITE 159 159 BY SIMILARITY.
 FT METAL 246 246 MAGNESIUM (BY SIMILARITY).
 FT METAL 289 289 MAGNESIUM (BY SIMILARITY).
 FT METAL 316 316 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 431 AA; 45686 MW; 3D7F1A0658328B12 CRC64;
 Query Match 9.4%; Score 88; DB 1; Length 431;
 Best Local Similarity 22.7%; Pred. No. 3.4;
 Matches 47; Conservative 34; Mismatches 78; Indels 48; Gaps 10;
 QY 3 NPVV--MVHGIGGASNFAGIKSVLSQGSRSGLYAVDFWDTGTNY-----N 49
 Db 18 NPTVEAEVHLEGG---FIGMAA--AFSGASTGSRLELRDGDGKSYLGKGLTAVANV 71
 QY 50 NGPVLRSFVKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGKNVENVVTLGGTNRSTT 109
 Db 72 NGPIRTALIGK--DATAQAELDQIMIDLDTEN---KDKLGANAI-LAVSLAAKAAAA 124
 QY 110 SKALP-----GTD-----ENOKILYTSIYSSADMVNVNLSKLDGAKVQIHGV 153
 Db 125 FGMFLYAHIAELNGTGPQYAVFPMNINLGGHADNNVDIOEFMVQPVGAKNFR---- 180
 QY 154 GHIGLLANNSOVNSLTKELNGGGGLNTN 180
 Db 181 --EALRMGAELFHTLKKVHLGKGLSIS 205
 RESULT 14
 BPHD PSES1
 ID BPHD PSES1 STANDARD; PRT; 277 AA.
 AC P17518;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (EC 3.7.1.-).
 GN BPHD.
 OS Pseudomonas sp. (strain KKS102).
 OC Bacteria; Proteobacteria.


```

OX NCBI_TaxID=307;
RN SEQUENCE FROM N.A.
RP STRAIN=Serotype 8;
RX MEDLINE=89213985; PubMed=2540155;
RA Kimbara K., Hashimoto T., Fukuda M., Koana T., Takagi M., Oishi M.,
RT Yano K.;
RT "Cloning and sequencing of two tandem genes involved in degradation
RT of 2,3-dihydroxybiphenyl to benzoic acid in the polychlorinated
RT biphenyl-degrading soil bacterium Pseudomonas sp. strain KKS102.";
RL J. Bacteriol. 171:2740-2747(1989).
CC -!- PATHWAY: Degradation of biphenyls and polychlorobiphenyls (PCB) to
CC benzoic acid and chlorobenzoic acids.
CC -!- SIMILARITY: STRONG, TO E.COLI MHP.
CC
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CC
CC EMBL; M26433; AAA25751.1; -
CC DR PIR; B32132; ESPSK.
CC DR InterPro; IPR000073; A/b_hydrolase.
CC DR InterPro; IPR003085; AB_hydrolase.
CC DR InterPro; IPR000379; Ser_estrfs.
CC DR Pfam; PF00561; abhydrolase; 1.
CC DR PRINTS; PR00111; ABHYDROLASE.
CC DR Aromatic hydrocarbons catabolism; Hydrolase.
CC ACT_SITE 112 BY SIMILARITY.
CC FT ACT_SITE 112
CC SEQUENCE 277 AA; 30253 MW; E0C7496186818D1E CRC64;
CC
Query Match 9.2%; Score 86; DB 1; Length 277;
Best Local Similarity 27.1%; Pred. No. 3;
Matches 42; Conservative 21; Mismatches 44; Indels 48; Gaps 9;
QY 5 VVMVHGIGGASFNFAGIKSVLSVSGWSR-----GKL-----YAVDFWPKTGTNNYNN----- 50
DB 36 VIMLHG-GGPG--AG-----GWSNYRNIGPFVEAGYRVLLPDAPGFNKSDFVWMD 83
QY 51 ---GPVLSRFVKYVLDGTGAKKVDIVAHSMGGANTLYIYKNDGGNKVENVTLGTNRS 107
DB 84 EQRGLVNRARSVKGMVDVLGIEKAHLVNSMGGAGALNFA--LEYPERTGKLILMG----- 136
QY 108 TTSKALPGTDPNQKILYTSIYSSADMIVMVLKSL 142
DB 137 -----PGG-----LGNSLFTAMPMEGIKLLFKL 159
RESULT 15
RT32 ACTPL STANDARD; PRT; 1052 AA.
AC P55131;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RTX-III toxin determinant A from serotype 8 (APX-IIIa) (Cytolysin
DE IIIA) (CLY-IIIa).
GN APXIIIa OR CLYIIIa OR RTXa OR PTXa.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=715;
RN SEQUENCE FROM N.A.
RP STRAIN=405 / Serotype 8;
RX MEDLINE=95012630; PubMed=7927703;
RA Jansen R., Briare J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
RA Smits M.A.;
RT "Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (ApX)
RT operons: characterization of the ApXIII operons.";
RL Infect. Immun. 62:4411-4418(1994).

```

```

[2] SEQUENCE FROM N.A.
RN RP STRAIN=Serotype 8;
RX MEDLINE=93162836; PubMed=8432615;
RA Jansen R., Briare J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
RT "Cloning and characterization of the Actinobacillus
RT pleuropneumoniae-RTX-toxin III (ApXIII) gene.";
RL Infect. Immun. 61:947-954(1993)
CC -!- FUNCTION: Does not have hemolytic activity but shows a strong
CC cytotoxicity towards alveolar macrophages and neutrophils.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: The Gly-rich region is probably involved in binding
CC calcium, which is required for target cell-binding or cytolytic
CC activity (By similarity).
CC -!- DOMAIN: The three transmembrane domains are believed to be
CC involved in pore formation by the cytotoxin (By similarity).
CC -!- PTM: Palmitoylated by apXIIIc. The toxin only becomes active when
CC modified (By similarity).
CC -!- SIMILARITY: Belongs to the RTX prokaryotic toxin family.
CC
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CC
CC EMBL; X80055; CAA56358.1; -
CC DR EMBL; X68815; CAA48711.1; -
CC DR PIR; B49219; B49219.
CC DR InterPro; IPR001343; Hemlysn_Ca_bind.
CC DR InterPro; IPR003995; RTXa.
CC DR Pfam; PF00353; hemolysinCbind; 6.
CC DR Pfam; PF02382; RTX; 1.
CC DR PRINTS; PR00313; CABDNDRPT.
CC DR PRINTS; PR01488; RTXTOXINA.
CC DR PROSITE; PS00330; HEMOLYSIN_CALCIUM; 3.
CC KW Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein;
CC Palmitate.
CC FT TRANSMEM 248 265
CC FT TRANSMEM 275 334
CC FT TRANSMEM 372 418
CC FT TRANSMEM 754 859
CC FT DOMAIN 754 759
CC FT REPEAT 763 768
CC FT REPEAT 772 777
CC FT REPEAT 781 786
CC FT REPEAT 790 795
CC FT REPEAT 799 804
CC FT REPEAT 808 813
CC FT REPEAT 827 832
CC FT REPEAT 836 841
CC FT REPEAT 845 850
CC FT REPEAT 854 859
CC FT REPEAT 854 859
CC SEQUENCE 1052 AA; 112809 MW; F83AFE25A6FD8758 CRC64;
CC
Query Match 9.2%; Score 86; DB 1; Length 1052;
Best Local Similarity 22.1%; Pred. No. 15;
Matches 33; Conservative 23; Mismatches 47; Indels 46; Gaps 7;
QY 41 WDKTGTNNNGFVLSRFVKYVLDGTGAKKVDIVAHSMGGANTLYIYKNDGGNKVENVVT 100
DB 922 WFEKGNKYNHK-----IEQIVDKNGRK--LTAENLG-----TYFKNAPKADNLLNVT 967
QY 101 LGGTRSTTSKALPGTDPNQKILYTSIYSSADMIVMVLKSLDGGKKNVQIHGVGHGL-- 158
DB 968 KEDQNESNLS-----SLKTELSKIITN-----AGNFGVAKQGTGINT 1005
QY 159 -LWNSQVNSLIKEG-----LNGGGLNT 179
DB 1006 AALNNEVNNKLISSANTFATSLQGGSGMGT 1034

```

us-09-905-666a-75.rsp

Mon Apr 26 08:04:04 2004

Search completed: April 23, 2004, 10:12:31
Job time : 10.1837 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:10:07 ; Search time 12.398 Seconds
(without alignments)
1396.558 Million cell updates/sec

Title: US-09-905-666A-75
Perfect score: 939
Sequence: 1 EHNPPVVMVHGIGASFNAG.....NSQVNSLIKEGLNGGLNTN 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: Pirl:.*
2: Pirl:.*
3: Pirl:.*
4: Pirl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	881	93.8	212	S23934	lipase lipA - Bacillus subtilis
2	714	76.0	210	S23934	lipase lipB - Bacillus subtilis
3	193	20.6	237	G75316	probable lipase -
4	170	18.1	290	T236757	probable secreted
5	156.5	16.7	202	S77556	hypothetical prote
6	144	15.3	211	A51975	hypothetical prote
7	134.5	14.3	300	T20712	hypothetical prote
8	134.5	14.3	371	T24853	hypothetical prote
9	133	14.2	286	T27932	hypothetical prote
10	130.5	13.9	344	T27932	triacylglycerol li
11	129.5	13.8	358	A48952	triacylglycerol li
12	126	13.4	479	A37027	hydrolase of alpha
13	121	12.9	292	T23322	hypothetical prote
14	120.5	12.8	474	B69470	lipase homolog - A
15	119.5	12.7	364	A39133	triacylglycerol li
16	118.5	12.6	364	JT0579	triacylglycerol li
17	116	12.4	335	T18906	hypothetical prote
18	116	12.4	340	T23812	hypothetical prote
19	115	12.2	171	S15911	hypothetical prote
20	115	12.2	333	T22227	hypothetical prote
21	114	12.1	339	C82486	lactonizing lipase
22	112.5	11.8	300	A01551	hypothetical prote
23	110.5	11.0	329	T24285	hypothetical prote
24	110	11.7	309	G83044	lipase LipC PA4813
25	110	11.7	323	T231927	lipase A precursor
26	106.5	11.3	277	T32460	hypothetical prote
27	105	11.2	488	A95301	hypothetical prote
28	103.5	11.0	497	H83886	hypothetical prote
29	102.5	10.9	1519	S41525	major ring-forming

30	102	10.9	281	2	T20894	hypothetical prote
31	96.5	10.3	309	2	D50879	hypothetical prote
32	96.5	10.3	309	2	H85529	hypothetical prote
33	96.5	10.3	681	2	G90075	triacylglycerol li
34	95.5	10.2	688	2	A47705	triacylglycerol li
35	95	10.1	267	2	F90316	esterase/lipase 1
36	94.5	10.1	299	2	T23932	hypothetical prote
37	94.5	10.1	303	1	E64762	probable 2,6-dioxo
38	94	10.0	237	2	T26860	hypothetical prote
39	93.5	10.0	299	2	Arl193	hypothetical prote
40	91	9.7	682	2	S68970	triacylglycerol li
41	90	9.6	662	2	S42826	probable ATPase -
42	89.5	9.5	690	2	A24545	triacylglycerol li
43	89.5	9.5	691	2	B89797	glycerol ester hyd
44	88.5	9.4	367	2	T49135	hypothetical prote
45	88.5	9.4	464	2	E72260	conserved hypothet

ALIGNMENTS

RESULT 1
S23934
lipase lipA - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999
C:Accession: S23934; B69652
R:Dartois, V.; Baulard, A.; Schanck, K.; Colson, C.
Biochim. Biophys. Acta 1131, 253-260, 1992
A:Title: Cloning, nucleotide sequence and expression in Escherichia coli of a lipase gen
A:Reference number: S23934; MUID:92329538; PMID:1320940
A:Accession: S23934
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-212 <DAB>
A:Cross-references: GB:M74010; NID:G143153; PIDN:AAA22574.1; PID:G143154
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, N.M.; Cho
A.; Ehrlich, S.D.; Emmer, P.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Pritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizai, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Takakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69652
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-132, 'L', 134-212 <KUN>
A:Cross-references: GB:T29105; GB:AL009126; NID:G2632457; PIDN:CAB12064.1; PID:ell182222;
A:Experimental source: strain 168
C:Genetics:
A:Gene: lipA
Query Match 93.8%; Score 881; DB 2; Length 212;
Best Local Similarity 93.3%; Pred. No. 2.1e-65;
Matches 168; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY	1	EHNPPVVMVHGIGASFNAGIKSYLVSCQWSKGLYAVDFWDTGTNTYNGVLSRFVKK	60
Db	33	EHNPPVVMVHGIGASFNAGIKSYLVSCQWSKGLYAVDFWDTGTNTYNGVLSRFVOK	92
QY	61	VLDGTGAKKVDIVAHSMGGANTLYIKNLGGNKVENVVLTGTTNRSTTSKALPGTDPNQ	120
Db	93	VLDGTGAKKVDIVAHSMGGANTLYIKNLGGNKVENVVLTGTTNRSTTSKALPGTDPNQ	152

A_Map position: 1

```
Query Match      20.6%; Score 193; DB 2; Length 237;
Best Local Similarity 29.1%; Pred. No. 1.1e-08;
Matches 55; Conservative 37; Mismatches 75; Indels 22; Gaps 5;

QY      3 NPVVMVHGIGASFNFAGIKSYLVISQGSWRGKLYAVDFWDKTGTNYNNGPVLGRFVKVL 62
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DBD     46 HPVLVFGHSDSGSIWSPMNRFPQDCWTDAQLFSWSY-DSFKSNAVTDALLRKVDAIL 104
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      63 DETGAKKVDIVAHSMGANTLYIKNLDDGKNVENVTLGTR-----STTS----- 110
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DBD     105 AQTGAARQVDIVSHSMGALSRRYILKNGGTAKVDAMVSLGSPNHGTFALACSTASCIEM 164
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      111 -----KAL-PGTRDPNQKILYTSIYSSADMIV-MNYLSKLDGAKNVCIHGVGHIGLLM 161
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      165 RQGSFFIKALNSGDSGTGCAVEYATWSPCDAVINPSSVPLSGATNTKTSCLTSSLYGD 224
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      162 SQVNSLIKE 170
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      225 ATVTQVRD 233
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
T36757
probable secreted lipase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
R:Accession: D36757
R:Saunders, D.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21613
A:Accession: T36757
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-290 <SAU>
A:Cross-references: EMBL:AL096849; PIDN:CAB50950.1; GSPDB:GN00070; SCODEB:SC11.24c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCODEB:SC11.24c

Query Match      18.1%; Score 170; DB 2; Length 290;
Best Local Similarity 29.2%; Pred. No. 1.1e-06;
Matches 56; Conservative 28; Mismatches 58; Indels 50; Gaps 8;

QY      4 PVVMVHGIGGASFNFAGIKSYLVISQGSWRGKLYAVDFWDKTGTN--YNGGPV-----L 54
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      56 PVVLVHGTFGNSVDNWLGLAPYLNKRGYC---VFLDTYGLFGVPLFGLGPEVKSASQL 112
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      55 SRFVKVLDITGAKKVDIVAHSMGANTLYIKNLDDGKNVENVTLGTRSTT-----S 110
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      113 AARVDKVLATGATGTEDLVGHSGGMPRYLKLGGAAEVNALVGIAPSNHGTTLSGLT 172
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      111 KALP-----GTPFNKILYTSIYSSADMIVMNYL 139
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      173 RLILPFPFGAEDLLNHTPALADQVVGSDVLTRLNAGGTVPGVRYTVLATKYDEVVTPYR 232
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      140 SK-LD--GAKNV 148
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      233 GQFLDGPGRNV 244
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
S77556
hypothetical protein sll1969 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
R:Accession: S77556
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, T.;
  O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yano
  DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
```

S:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S77556
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-202 <RAN>
 A:Cross-references: EMBL:D90905; GB:AB001339; NID:G1852360; PIDN:BAAL7403.1; PID:d101813
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Start codon: GTG

	Query Match	16.7%	Score 156.5	DB 2	Length 202
	Best Local Similarity	32.7%	Fred. No. 9e-06		
	Matches	36	Conservative	24	Mismatches 43
					Indels 7
					Gaps 3
Qy	1	EHPVVMVHGIGGASFNFAIGKSYLVSQGHSRGLYAVDFMDKTGTNNNGNPVLRSFVKK	60		
Db	7	DRHPVVLVHGIIYTRAKFAFMVDFLTGKGWS---	VHCLDLVPNDGS--	TSLALLASQVKQ	61
Qy	61	VLDETGA--KKVDIVAHSMGGANTLYIKNLGDGNKVENVVTLLGGTNRST	108		
Db	62	YIDOKFAPOQPVLLIGFSMGGLVTRYVYLOBLGGGERVRRYITISAPNQST	111		

RESULT 6

AE1975
hypothetical protein alr1352 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE1975
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Kanezaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1975
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <CUR>
A:Cross-References: GB:BA000019; PIDN:BAE73309.1; PID:gl7130699; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr1352

Query Match	15.38;	Score 144;	DB 2;	Length 211;
Best Local Similarity	26.57;	Fred.No. 0.0000;		
Matches	54;	Conservative	76;	Indels 40; Gaps 8;
Qy	1	EHNPVNVHIGIGGASFNPAIGIKSYLVYQGSWSRGLKYAVDFWDMGTGTNNYNGPV-LSRFVK	59	
Db	7	ORNPVLLVHGITDTETVFNPMAVYRGLGVTVTNLVP-----NNGEAPLVNLAQ	57	
Qy	60	KVLDE-----TGAKKVDIVAHSGGANTLYIKNLGGNKVENVTLGGTNRRT---SK	111	
Db	58	QVADYVCATITPEQFDLVGFSMGIVSYRYVVKLGGISVQRFVITSSPHHGTVVAYAS	117	
Qy	112	ALPG-----TDNF-----QXILYTSIYSASD-MIVMNYLSKLDGAKNVTHGV	153	
Db	118	QHPGCVQMRENSLFLOQLNRDVQMLEQLNFTSIWTPYDLMIPTHSKMPVGKELTPVA	177	
Qy	154	GHIGLLMN-----SOVNSLIKEGLN	173	
Db	178	LHSMMLKDFRSIEAVAAALAEPPIN	201	

RESULT 7
T20712
hypothetical protein F102.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T20712
R:Coles, L.

submitted to the EMBL Data Library, August 1994
A;Reference number: Z19313
A;Accession: T20712
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1300 <WIL>
A;Cross-references: EMBL:Z35598; PTDN:CA84650.1; GSPDB:GN00021; CESP:F10F2.3
A;Experimental source: clone F10F2
C;Genetics:
A;Gene: CESP:F10F2.3
A;Map position: 3
A;Introns: 13/2, 115/2, 208/3, 268/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C09E8.2

Query Watch	14.3%;	Score 134.5;	DB 2;	Length 300;
Best Local Similarity	25.7%;	Pred. No. 0.00096;		
Matches	47;	Conservative 21;	Mismatches 64;	Indels 51; Gaps 6

QY	1	EHNPVVWTHGTGGASF-----	NRAGIKSYLVSGNSRGKLYAVDPWDKTGT-----	46
DB	41	EXEPIFPIHFGSGDALTFTQPLATGFSRSIQYLEONYTEAEIYATTGDTWGGSM	LDLT	100
QY	47	-----	NYNNGPVLSRFPVKVLDEGAKVDIVAHSMGGANTLIYYIK-----	91
DB	101	YSTHTTCGNLIYLRRELEAVIGYTGAKKVDIIIAHSGVPLMRKVKGGLITDGNCT	ILG	160
QY	92	---GNKVENVVTLGTTNRS-----	TTSKALPGTDPNPKILYTSIYSSADMVNN	137
DB	161	PPLGAKVDTFTFLGIAGPNFGLVCQLAQTPAWCNALDGLYP-----	YTCDQLMGCG	212
QY	138	YLS	140	
DB	213	YTS	215	

RESULT 8
T24853
Hypothetical protein T12A7.4 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T24853
R/Lennard, N.
submitted to the EMBL Data Library, June 1996
A/Reference number: Z19943
A/Accession: T24853
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-371 xwIL>
A/Cross-references: EMBL:Z73911; PIDN:CAA98139.1; GSPDB:GNO0022; CESP:T12A7.4
A/Experimental source: clone T12A7
C/Genetics:
A/Gene: CESP:T12A7.4
A/Map position: 4
A/Introns: 105/3; 139/3; 166/2; 218/1; 261/3; 318/1; 343/3

[illegible]

RESULT 9

T26657
hypothetical protein Y38E10A.g - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T26657
R:Wallis, J.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z20252
A:Accession: T26657
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <WIL>
A:Cross-references: EMBL:AL110484; PIDN:CA854398.1; CESP:Y38E10A.g
A:Experimental source: clone Y38E10A
C:Genetics:
A:Gene: CESP:Y38E10A.g
A:Introns: 63/2; 221/2; 261/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C09E8.2

Query Match 14.2%; Score 133; DB 2; Length 286;
Best Local Similarity 25.4%; Pred. No. 0.0012;
Matches 49; Conservative 25; Mismatches 65; Indels 54; Gaps 7;

QY 4 PVVMVHGIGGASFNAGKSYLVSGWSRGKLYAVDFWDKTGTNNYNGPVLSPFVKV-- 61
DB 66 PVILVHGTTNSAGTAPQAAYFRANGNSEETVYATTYDAGVTTATNVKMLCEYVQGIN 125
QY 62 ---LDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVTLG-----G 103
DB 126 MLIANVATQKXNVIGSMSPAR---KAILGGKCAENVQLGAPLTSIIETIYSVAG 182
QY 104 TNRST-----TSKALPG-----TDPNQKILYT-----SIYSSAD----- 132
DB 183 ANRGTSLCDILPAPLWPTCTNKLKGSDFLDIRSVAYEGQYIFSIYGPSDDXVGF 242
QY 133 MIVMYLKLQGA 145
DB 243 NTVGGRVSKIDGA 255

RESULT 10
T27932
hypothetical protein ZK617.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27932
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20442
A:Accession: T27932
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-344 <WIL>
A:Cross-references: EMBL:Z73897; PIDN:CAA98062.1; GSPDB:GN00022; CESP:ZK617.2
A:Experimental source: clone ZK617
C:Genetics:
A:Gene: CESP:ZK617.2
A:Map position: 4
A:Introns: 62/2; 121/3; 288/2

Query Match 13.9%; Score 130.5; DB 2; Length 344;
Best Local Similarity 25.9%; Pred. No. 0.0024;
Matches 52; Conservative 27; Mismatches 71; Indels 51; Gaps 9;

QY 4 PVVMVHGIGGASFNAGKSYLVSGWSRGKLYAVDFWDKTGTNNYNGPVLSPVLS----- 55
DB 65 PVFVHGLNAGSLWKIARDFTNANYPQYLFATT-WKGTEPLNLNVAMSCTHVQVR 123
QY 56 RFVKVLDGTGAKKVDIVAHSMGGANTLYYI---KNLGGN-----KYENVVTLGG 103
DB 124 RFETVLKYGAKIDVIGSMSPARAKILGGKVDNPNVALGSLHSRVHTIYSVAG 183
QY 104 TNRSTTSKALP-----GTDPNQKIL-----YTSIY-----SSADMIVNYL- 139

Db 184 ANQGSQCALPFFDICNMKTKGLMCKSKFLEDINWFKNTYEGSKAFNLTADFFV-GYMA 242
QY 140 -----SKLDGAKNVQIHGVGH 155
DB 243 CGKKASEFTGAHEWKVEGRNH 263

RESULT 11
A49952
triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas glumae
C:Species: Pseudomonas glumae
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49952; S36248; S37291
R:Freken, L.G.J.; Bos, J.W.; Viesser, C.; Tomassen, J.; Verrips, C.T.
Appl. Environ. Microbiol. 58, 3787-3791, 1992
A:Title: Cloning of the Pseudomonas glumae lipase gene and determination of the active site
A:Reference number: A49952; MUID:93119130; PMID:1476423
A:Accession: A49952
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <PRE>
A:Cross-references: EMBL:X70354; NID:G49205; PIDN:CAA49812.1; PID:G49206
A:Experimental source: PGI
A:Note: sequence extracted from NCBI backbone (NCBIN:121572, NCBI:121573)
R:Freken, L.G.J.; Bos, J.W.; Viesser, C.; Mueller, W.; Tomassen, J.; Verrips, C.T.
Mol. Microbiol. 9, 579-585, 1993
A:Title: An accessory gene, lipB, required for the production of active Pseudomonas glum
A:Reference number: S36248; MUID:94018652; PMID:8412704
A:Accession: S36248
A:Molecule type: DNA
A:Residues: 316-358 <FR2>
A:Cross-references: EMBL:X70354
C:Genetics:
A:Gene: lipA
C:Superfamily: Pseudomonas triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase; extracellular protein

Query Match 13.8%; Score 129.5; DB 1; Length 358;
Best Local Similarity 34.8%; Pred. No. 0.0031;
Matches 40; Conservative 16; Mismatches 42; Indels 17; Gaps 6;

QY 4 PVVMVHGIGGASFNFA-----GIKSYLVSGWSRGKLYAVD---FWDKTGTNNYNGPV 53
DB 49 PVILVHGLAGTD-KPANVVDYVYGIQSDLSHG---AKYVANLSGFQDDGPN-GRGQ 103
QY 54 LSRFVKVLDGTGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVTLGTTNRST 108
DB 104 LLAYVKQVLAATGATKVNLIHSGQGLTSRYVA--AVAPQVASVTITGTPHRGS 156

RESULT 12
A97027
hydrolase of alpha/beta superfamily, probable membrane associated lipase [imported] - Cl
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: A97027
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: A97027
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK79004.1; PID:GI5023939; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1028

Query Match 13.4%; Score 126; DB 2; Length 479;
Best Local Similarity 22.0%; Pred. No. 0.0086;

Matches 54; Conservative 38; Mismatches 65; Indels 88; Gaps 12;
QY 4 PVMVHGIGGAS---FNFAG-IKSVLVSGWGRGKLY--AVDFWKTGTNTYNNNGPVLRSF 57
DB 223 PLVLVHGVRDLKYINWGRIPKELIRNG---ATIIYGNQEA---GTVEYNAQYMKK 276
QY 58 VRKVLDETCAGKVDIVAHSMGGANTLYIYIKNLDGNGKVENVVTGGTNR----- 106
DB 277 ILQIIKETCEKNIITAHSGGLGDSRYWYKLEMGKYVASLTWMSGPHRGCKFVDIACKI 336
QY 107 -----SITS-----KALPGTDPNOKILYT 125
DB 337 PDKIYRAVNFFDKYKILGDKNPDFTASRFSFVSYSKFNVEKDVPG-----VYIQ 390
QY 126 SIYSSADMTWNY-----LSKL-----DGAKNQIHGCVHI-GLLMNSQVNSLIKEGL 172
DB 391 SYATAKNTFSDVVSIPYVLKLTSGENDGLVLSIDSAKWGHFKGVIRNR-----RSGI 445
QY 173 NGGGL 177
DB 446 SHGDI 450
RESULT 13
T33322
hypothetical protein C09E8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
C:Accession: T33322
R:Du, Z.; Graves, T.; Gibson, A.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of Caenorhabditis elegans cosmid C09E8.
A:Reference number: Z21322
A:Accession: T33322
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-292 <DUZ>
A:Cross-references: EMBL:AF077529; PIDN:AA26254.1; GSPDB:GN00020; CESP:C09E8.2
A:Experimental source: strain Bristol N2; clone C09E8
C:Genetics:
A:Gene: CESP:C09E8.2
A:Map position: 2
A:Introns: 80/3; 123/2; 166/1; 200/2
C:Superfamily: Caenorhabditis elegans hypothetical protein C09E8.2
Query Match 12.9%; Score 121; DB 2; Length 292;
Best Local Similarity 25.4%; Pred. No. 0.012;
Matches 44; Conservative 25; Mismatches 58; Indels 46; Gaps 6;
QY 3 NPVMVHGIGGASFNAGIKSVLVSGWGRGKLYAVDFWDKTGTNTYNNNGPVLRSFVKV- 61
DB 64 NPVLIVHGITNKASRFGCTVAYLKSKYKSEIYGTWGDGRTPGVLVDMKCNVYKQIR 123
QY 62 -----LDETCAGKVDIVAHSMGGANTLYIYIKNLDGNGKVENVVTLG----- 102
DB 124 AMIIVAVRQYTGQKVDVIGYSNGSPLAR---KAILGGQCVDTREILGAPLTVDLTSLVA 180
QY 103 GTNRSTTSKALP---GT-----DPNQKILYT-----SIYSSAD 132
DB 181 GANYGSVLCILFVPGVGTCKNKGHLHCDSFELQDINNQHRYEGSHVFSIFSTAD 233
RESULT 14
B69470
lipase homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Jun-2000
C:Accession: B69470
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: B69470
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-474 <KLE>
A:Cross-references: GB:AE000981; GB:AE000782; NID:g2689304; PIDN:AA889488.1; PID:g264878.
C:Superfamily: Archaeoglobus fulgidus probable lipase AF1763

Query Match 12.8%; Score 120.5; DB 2; Length 474;
Best Local Similarity 20.7%; Pred. No. 0.024;
Matches 48; Conservative 37; Mismatches 66; Indels 81; Gaps 9;
QY 1 EHNPMVVMHGIGGASFNAGIKSVLVSGWGRGKLYAVDF-----W-----D 42
DB 21 DFRDVFVHVLGASAGQFESQGMRFAGYPAEYVKTTFEYDTISWALVWETDMLFSLGSG 80
QY 43 KTGTNNY-----GPVLSRFVKVKLDET-----GAKKVDIVAHSMGGA 80
DB 81 EFGNISQIIDPETLDKILSKSERLIDETFSRLDRVIDEALAESGADKVDLVCHSNGTG 140
QY 81 NTLYYIKNL-DGNGKVENVVTLGST-----NRSTTSKALPGTD-PNQKI 122
DB 141 FLVRYVNSSPERAAKVAHLILLDGVWGVDAPGEGIPTLAVFGN---PKALPALGLPEEKV 196
QY 123 LYTSIYSSADMVNNYLSKLDGAKNQIHGCVHIGLGLMNSQVNSLIKEGLNG 174
DB 197 VY-----NATNVYNNNTHVOLCTSPETFAVMFEFING 229

RESULT 15
A39133
triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas cepacia
C:Species: Pseudomonas cepacia
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A39133
R:Jorgensen, S.; Skov, K.W.; Diderichsen, B.
J. Bacteriol. 173, 559-567, 1991
A:Title: Cloning, sequence, and expression of a lipase gene from Pseudomonas cepacia: 1;
A:Reference number: A39133; MUID:91100343; PMID:1987151
A:Accession: A39133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <JOK>
A:Cross-references: GB:M58494
C:Superfamily: Pseudomonas triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase

Query Match 12.7%; Score 119.5; DB 1; Length 364;
Best Local Similarity 29.9%; Pred. No. 0.021;
Matches 35; Conservative 19; Mismatches 42; Indels 21; Gaps 6;
QY 4 PVMVHGIGGASFNAGIKSVLVSGW-----SRGKLYAVD---FWDKGTNTYNNNG 51
DB 54 PIILVHGLSGTD-KYAGVLEY-----WYGIQEDLQONGATVYVANLSGFSQDDGPN-GRG 106
QY 52 PVLRSFVKVKLDETGAKKVDIVAHSMGGANTLYIYIKNLDGNGKVENVVTGGTNRST 108
DB 107 BOLLAYVKTVLAATGATKVLNVGHSGGSLSSRYVA--AVAPDLVASVTTIGPADRGS 161

Search completed: April 23, 2004, 10:15:21
Job time : 13.398 secs

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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:14:03 ; Search time 35.3571 Seconds

(without alignments)
1407.510 Million cell updates/sec

Title: US-09-905-666A-75

Perfect score: 939
Sequence: 1 EHNPMVVMHIGGASFNAG.....NSQVNSLIKEINGGGLNTN 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA**

- 1: /cgn2_5/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	939	100.0	180	US-09-905-666A-75
2	927	98.7	180	US-09-905-666A-104
3	925	98.5	180	US-09-905-666A-78
4	924	98.4	180	US-09-905-666A-98
5	923	98.3	180	US-09-905-666A-76
6	923	98.3	180	US-09-905-666A-108
7	922	98.2	180	US-09-905-666A-87
8	920	98.0	180	US-09-905-666A-77
9	920	98.0	212	US-09-905-666A-58
10	920	98.0	212	US-09-905-666A-59
11	920	98.0	212	US-10-028-247-4
12	919	97.9	180	US-09-905-666A-99
13	917	97.7	180	US-09-905-666A-82
14	917	97.7	180	US-09-905-666A-107
15	914	97.3	180	US-09-905-666A-102

16	913	97.2	180	US-09-905-666A-103	Sequence 103, App
17	913	97.2	180	US-09-905-666A-105	Sequence 105, App
18	913	97.2	212	US-09-905-666A-62	Sequence 62, App
19	912	97.1	180	US-09-905-666A-81	Sequence 81, App
20	911	97.0	180	US-09-905-666A-100	Sequence 100, App
21	911	97.0	180	US-09-905-666A-101	Sequence 101, App
22	909	96.8	212	US-09-905-666A-55	Sequence 55, App
23	909	96.8	212	US-09-905-666A-61	Sequence 61, App
24	907	96.6	180	US-09-905-666A-97	Sequence 97, App
25	906	96.5	180	US-09-905-666A-86	Sequence 86, App
26	906	96.5	180	US-09-905-666A-88	Sequence 88, App
27	906	96.5	212	US-09-905-666A-60	Sequence 60, App
28	905	96.4	180	US-09-905-666A-94	Sequence 94, App
29	904	96.3	180	US-09-905-666A-106	Sequence 106, App
30	902	96.1	180	US-09-905-666A-80	Sequence 80, App
31	902	96.1	180	US-09-905-666A-84	Sequence 84, App
32	901	96.0	180	US-09-905-666A-85	Sequence 85, App
33	897	95.5	180	US-09-905-666A-83	Sequence 83, App
34	895	95.3	180	US-09-905-666A-96	Sequence 96, App
35	891	94.9	180	US-09-905-666A-89	Sequence 89, App
36	889	94.7	180	US-09-905-666A-95	Sequence 95, App
37	887	94.5	180	US-09-905-666A-90	Sequence 90, App
38	887	94.5	180	US-09-905-666A-93	Sequence 93, App
39	886	94.4	212	US-09-905-666A-69	Sequence 69, App
40	882	93.9	212	US-09-905-666A-63	Sequence 63, App
41	881	93.8	180	US-09-905-666A-91	Sequence 91, App
42	881	93.8	212	US-09-905-666A-56	Sequence 56, App
43	880	93.7	180	US-09-905-666A-92	Sequence 92, App
44	872	92.9	212	US-09-905-666A-70	Sequence 70, App
45	869	92.5	212	US-09-905-666A-68	Sequence 68, App

ALIGNMENTS

RESULT 1
US-09-905-666A-75
; Sequence 75, Application US/0905666A
; Publication No: US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184,310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 75
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-75

Query Match	100.0%;	Score 939;	DB 10;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 6.1e-93;	Mismatches 0;	Indels 0;
Matches 180;	Conservative 0;			
QY	1	EHNPMVVMHIGGASFNAGIKSVLSQGWGRGKLYAVDFWDTGTGTYNNYNGPVLRSFYKK	60	
Db	1	EHNPMVVMHIGGASFNAGIKSVLSQGWGRGKLYAVDFWDTGTGTYNNYNGPVLRSFYKK	60	
QY	61	VLDTCAGKVDIVAHSMGGANTLYIIRKLDGNGKVENVTLLGGTNRSTTSKALGTDPNQ	120	
Db	61	VLDTCAGKVDIVAHSMGGANTLYIIRKLDGNGKVENVTLLGGTNRSTTSKALGTDPNQ	120	

Qy 121 KILTSYSSADMTWNYLSKLDGAKNQVTHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

Db 121 KILTSYSSADMTWNYLSKLDGAKNQVTHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 2

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US-09-905-666A-104
; Sequence 104, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184 310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-104

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REF ID: A66123

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RES001 3
US-09-905-666A-78
; Sequence 78, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2002-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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RECEIVED

US-09-905-666A-76
; Sequence 76, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSCHULL, JEREMY
; APPLICANT: VOGEL, KURT

; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-76

Query Match
Best Local Similarity 98.3%; Score 923; DB 10; Length 180;
Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EHNPMVVMHIGIGGASFNFAGIKSYLVSQWRSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 60
DB 1 EHNPMVVMHIGIGGASFNFAGIKSYLVSQWRSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKD 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYIYKNDGCKNKENVVTLLGGANRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYIYKNDGCKNKENVVTLLGGANRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 6
US-09-905-666A-108
; Sequence 108, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-108

Query Match
Best Local Similarity 98.3%; Score 923; DB 10; Length 180;
Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EHNPMVVMHIGIGGASFNFAGIKSYLVSQWRSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 60
DB 1 EHNPMVVMHIGIGGASFNFAGIKSYLVSQWRSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKQ 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYIYKNDGCKNKENVVTLLGGANRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYIYKNDGCKNKENVVTLLGGANRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

DB 61 VLDETGAKKVDIVAHSMGGANTLYIYKNDGCKNKENVVTLLGGANRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 7
US-09-905-666A-87
; Sequence 87, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-87

Query Match
Best Local Similarity 98.2%; Score 922; DB 10; Length 180;
Matches 175; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EHNPMVVMHIGIGGASFNFAGIKSYLVSQWRSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKK 60
DB 1 EHNPMVVMHIGIGGASFNFAGIKSYLVSQWRSRGKLYAVDFWDTGTNTYNNNGPVLRSFVKQ 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYIYKNDGCKNKENVVTLLGGANRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYIYKNDGCKNKENVVTLLGGANRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 8
US-09-905-666A-77
; Sequence 77, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-905-666A-77

Query Match 98.0%; Score 920; DB 10; Length 180;
Best Local Similarity 97.2%; Pred. No. 6.5e-91;
Matches 175; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTGTYNNGPVLRSFVKK 60
DB 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTGTYNNGPVLRSFVKK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGGANRLTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 9

US-09-905-666A-58
Sequence 58, Application US/09905666A
Publication No. US20030096390A1
GENERAL INFORMATION:
APPLICANT: GIVER, LORRAINE J.
APPLICANT: MINSHULL, JEREMY
APPLICANT: VOGEL, KURT
TITLE OF INVENTION: NOVEL LIPASE GENES
FILE REFERENCE: 0184.310US
CURRENT APPLICATION NUMBER: US/09/905.666A
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 2000-07-13
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/300,378
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 58
LENGTH: 212
TYPE: PRT
ORGANISM: Bacillus lentus
US-09-905-666A-58

Query Match 98.0%; Score 920; DB 10; Length 212;
Best Local Similarity 97.2%; Pred. No. 8.5e-91;
Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTGTYNNGPVLRSFVKK 60
DB 33 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTGTYNNGPVLRSFVKK 92
QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGGTNRSTTSKALPGTDPNQ 120
DB 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGGANRLTTSKALPGTDPNQ 152
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 153 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 212

RESULT 10

US-09-905-666A-59
Sequence 59, Application US/09905666A
Publication No. US20030096390A1
GENERAL INFORMATION:
APPLICANT: GIVER, LORRAINE J.
APPLICANT: MINSHULL, JEREMY
APPLICANT: VOGEL, KURT
TITLE OF INVENTION: NOVEL LIPASE GENES
FILE REFERENCE: 0184.310US

CURRENT APPLICATION NUMBER: US/09/905.666A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/217,954
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/300,378
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 59
LENGTH: 212
TYPE: PRT
ORGANISM: Bacillus circulans
US-09-905-666A-59

Query Match 98.0%; Score 920; DB 10; Length 212;
Best Local Similarity 97.2%; Pred. No. 8.5e-91;
Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTGTYNNGPVLRSFVKK 60
DB 33 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTGTYNNGPVLRSFVKK 92
QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGGTNRSTTSKALPGTDPNQ 120
DB 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGGANRLTTSKALPGTDPNQ 152
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 153 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 212

RESULT 11

US-10-028-247-4
Sequence 4, Application US/10028247
Publication No. US20020150594A1
GENERAL INFORMATION:
APPLICANT: Goldman, Stanley
APPLICANT: Iathrop, Stephanie J.
APPLICANT: Longchamp, Pascal F.
APPLICANT: Whalen, Robert G.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Methods and Compositions for Developing Spore Display
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
FILE REFERENCE: 18097A-033520US
CURRENT APPLICATION NUMBER: US/10/028.247
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/214,161
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 09/892,208
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 4
LENGTH: 212
TYPE: PRT
ORGANISM: Bacillus circulans
FEATURE: lipase 396
OTHER INFORMATION: lipase 396
US-10-028-247-4

Query Match 98.0%; Score 920; DB 13; Length 212;
Best Local Similarity 97.2%; Pred. No. 8.5e-91;
Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTGTYNNGPVLRSFVKK 60
DB 33 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDTGTGTYNNGPVLRSFVKK 92
QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGGTNRSTTSKALPGTDPNQ 120
DB 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLGGANRLTTSKALPGTDPNQ 152
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

Db 153 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 212
|||||
RESULT 12
US-09-905-666A-99
; Sequence 99, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-99
Query Match 97.9%; Score 919; DB 10; Length 180;
Best Local Similarity 97.2%; Pred. No. 8.7e-91;
Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EHNPMVVMHIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTGTNNNGPVLRSFVKK 60
Db 1 EHNPMVVMHIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTGTNNNGPVLRSFVKK 60
Qy 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVVLGGTNRSTTSKALPGTDPNQ 120
Db 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKIENVVLGGANRSTTSKALPGTDPNQ 120
Qy 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
Db 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGHNTN 180
RESULT 13
US-09-905-666A-82
; Sequence 82, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-82
Query Match 97.7%; Score 917; DB 10; Length 180;
Best Local Similarity 97.8%; Pred. No. 1.4e-90;
Matches 176; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EHNPMVVMHIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTGTNNNGPVLRSFVKK 60
Db 1 EHNPMVVMHIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTGTNNNGPVLRSFVKK 60
Qy 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVVLGGTNRSTTSKALPGTDPNQ 120
Db 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKIENVVLGGANRSTTSKALPGTDPNQ 120
Qy 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
Db 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGHNTN 180
RESULT 14
US-09-905-666A-107
; Sequence 107, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-107
Query Match 97.7%; Score 917; DB 10; Length 180;
Best Local Similarity 97.8%; Pred. No. 1.4e-90;
Matches 176; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EHNPMVVMHIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTGTNNNGPVLRSFVKK 60
Db 1 EHNPMVVMHIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTGTNNNGPVLRSFVKK 60
Qy 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVVLGGTNRSTTSKALPGTDPNQ 120
Db 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKIENVVLGGANRSTTSKALPGTDPNQ 120
Qy 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
Db 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 180
RESULT 15
US-09-905-666A-102
; Sequence 102, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US

US-09-905-666A-82
Query Match 97.7%; Score 917; DB 10; Length 180;
Best Local Similarity 96.7%; Pred. No. 1.4e-90;
Matches 174; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EHNPMVVMHIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTGTNNNGPVLRSFVKK 60
Db 1 EHNPMVVMHIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTGTNNNGPVLRSFVKK 60
Qy 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVVLGGTNRSTTSKALPGTDPNQ 120
Db 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKIENVVLGGANRSTTSKALPGTDPNQ 120
Qy 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
Db 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
RESULT 14
US-09-905-666A-107
; Sequence 107, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-107
Query Match 97.7%; Score 917; DB 10; Length 180;
Best Local Similarity 97.8%; Pred. No. 1.4e-90;
Matches 176; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EHNPMVVMHIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTGTNNNGPVLRSFVKK 60
Db 1 EHNPMVVMHIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTGTNNNGPVLRSFVKK 60
Qy 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVVLGGTNRSTTSKALPGTDPNQ 120
Db 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKIENVVLGGANRSTTSKALPGTDPNQ 120
Qy 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
Db 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 180
RESULT 15
US-09-905-666A-102
; Sequence 102, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US

; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-905-666A-102

Query Match 97.3%; Score 914; DB 10; Length 180;
Best Local Similarity 96.7%; Pred. No. 3e-90;
Matches 174; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EHNPPVVMVHGIGGASFNFAIGKISYLVSGWSRGLYAVDFWMDKTGTNNNGFVLSRFVKK 60
Db 1 EHNPPVVMVHGIGGASFNFAIGKISYLVSGWSRGLYAVDFWMDKTGTNNNGFVLSRFVKK 60
QY 61 VLDETGAKKVDIVAHSGGANTLYIKNLGGKNKVENVVTLCGTNRSTTSKALPGTDNQ 120
Db 61 VLDETGAKKVDIVAHSGGANTLYIKNLGGKNKVENVVTLCGTNRSTTSKALPGTDNQ 120
QY 121 KILYTSYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
Db 121 KILYTSYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180

Search completed: April 23, 2004, 10:23:29
Job time : 36.3571 secs

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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:08:37 ; Search time 15.1531 Seconds
(without alignments)
613.254 Million cell updates/sec

Title: US-09-905-666A-75
Perfect score: 939
Sequence: 1 ENPVMVHGICGASNFAG.....NSQVNSLIKEGLNGGLNTN 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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5: /cgn2_6/prodata/2/1aa/PCITUS-COMB.pap:*
6: /cgn2_6/prodata/2/1aa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	747	79.6	213	1	US-07-930-678-2
2	129.5	13.8	358	1	US-08-034-650-10
3	129.5	13.8	358	1	US-08-449-015-10
4	117.5	12.5	363	3	US-08-978-589A-2
5	117.5	12.5	363	3	US-09-336-601-1
6	117.5	12.5	363	4	US-09-219-120-2
7	110.5	11.8	296	4	US-09-543-681A-7771
8	110.5	11.8	364	1	US-08-400-422-3
9	110	11.7	351	4	US-09-252-991A-27337
10	107.5	11.4	318	4	US-09-489-039A-7418
11	97.5	10.4	690	4	US-09-134-001C-4568
12	95.5	10.2	699	4	US-09-134-001C-4054
13	94.5	10.1	299	4	US-09-584-568C-5
14	93.5	10.0	292	4	US-09-134-001C-3301
15	92.5	9.9	308	4	US-09-584-568C-8
16	92	9.8	316	4	US-09-107-532A-4594
17	90.5	9.6	325	4	US-09-328-352-6196
18	87.5	9.3	1216	4	US-09-134-000C-5130
19	86.5	9.2	388	1	US-08-232-519-2
20	86.5	9.2	388	1	US-08-456-956-2
21	86	9.2	264	4	US-09-134-001C-5592
22	86	9.2	1053	4	US-09-062-126-10
23	85.5	9.1	453	4	US-09-328-352-5069
24	85	9.1	652	4	US-09-134-001C-3517
25	84.5	9.0	416	4	US-09-489-039A-8245
26	84	8.9	262	2	US-08-602-359A-35
27	83.5	8.9	315	4	US-09-584-568C-2

28 83 8.8 284 4 US-09-134-001C-2927 Sequence 2927, Ap
29 83 8.8 491 4 US-09-134-001C-3510 Sequence 3510, Ap
30 83 8.8 503 4 US-09-562-737-64 Sequence 64, Appl
31 82.5 8.8 236 4 US-09-134-000C-5155 Sequence 5155, Ap
32 82 8.7 734 4 US-09-489-039A-9951 Sequence 9951, Ap
33 82 8.7 1059 4 US-09-489-039A-10044 Sequence 10044, A
34 81.5 8.7 277 3 US-09-111-556A-3 Sequence 3, Appli
35 81.5 8.7 277 3 US-08-360-758-3 Sequence 2, Appli
36 81 8.6 313 3 US-08-732-412-2 Sequence 2, Appli
37 81 8.6 671 2 US-08-737-716-13 Sequence 13, Appli
38 81 8.6 700 4 US-09-620-412C-345 Sequence 345, App
39 81 8.6 700 4 US-09-598-419-345 Sequence 345, App
40 81 8.6 1752 4 US-09-556-877-180 Sequence 180, App
41 81 8.6 1752 4 US-09-620-412C-180 Sequence 180, App
42 81 8.6 1752 4 US-09-598-419-180 Sequence 180, App
43 80.5 8.6 464 4 US-09-711-164-441 Sequence 441, App
44 80.5 8.6 766 4 US-09-540-236-2515 Sequence 2515, Ap
45 80.5 8.6 1221 4 US-09-107-532A-3959 Sequence 3959, Ap

ALIGNMENTS

RESULT 1
US-07-930-678-2
; Sequence 2, Application US/07930678
; Patent No. 5427936
; GENERAL INFORMATION:

APPLICANT: MOELLER, Bernhard
APPLICANT: VETTER, Roman
APPLICANT: WILKE, Detlef
APPLICANT: FOULLOIS, Birgit
TITLE OF INVENTION: Alkaline Bacillus Lipases, Coding DNA
Sequences Therefor and Bacilli, Which Produce These
TITLE OF INVENTION: Lipases
TITLE OF INVENTION: Lipases
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/930,678
FILING DATE: 19921013
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP91/00664
FILING DATE: 08-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12 070.8
FILING DATE: 14-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, J.D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 16877/318/KACH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-930-678-2

QY 54 LSRFVKKVLDETGAKKVDIVAHSMGGANTLYYIKNLDDGKNKVENVTTLGGTNRST 108
Db 104 LLAYVKQVLAATGATKVNLIHSGGLTSRYVA--AVAPQLVASVTITGTPHRGS 156

RESULT 3

US-08-449-015-10
; Sequence 10, Application US/08449015
; Patent No. 5804409
; GENERAL INFORMATION:
; APPLICANT: BOS, Jannetje W.
; APPLICANT: FRENKEN, Leon G.
; APPLICANT: VERRIJS, Cornelis T.
; APPLICANT: VISSER, Christiaan
; TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
; TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/449,015
; APPLICATION NUMBER: US 07/727,235
; FILING DATE: 03-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PNK/5970/91731
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-015-10

Query Match 13.8%; Score 129.5; DB 1; Length 358;
Best Local Similarity 34.8%; Pred. No. 9.7e-06;
Matches 40; Conservative 16; Mismatches 42; Indels 17; Gaps 6;

QY 4 PVTVMHIGGASNF-----GIKSYLVSGWSRGKLYAVD---FWDKTTGTNNNGPV 53
Db 49 PVLVHGLAGTD-KFANVVDYWGIDSLQSHG---AKVIVANLSGFQSDGPN-GRGEQ 103
QY 54 LSRFVKKVLDETGAKKVDIVAHSMGGANTLYYIKNLDDGKNKVENVTTLGGTNRST 108
Db 104 LLAYVKQVLAATGATKVNLIHSGGLTSRYVA--AVAPQLVASVTITGTPHRGS 156

RESULT 4

US-08-578-589A-2
; Sequence 2, Application US/08978589A
; Patent No. 6087145
; GENERAL INFORMATION:
; APPLICANT: ISHII, Takeshi
; APPLICANT: MITSUDA, Satoshi
; TITLE OF INVENTION: ESTERASE GENE AND ITS USE

Query Match 79.6%; Score 747; DB 1; Length 213;
Best Local Similarity 78.3%; Pred. No. 5.2e-73;
Matches 141; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

QY 1 EHNPFVWHGIGGASNFAGIKSYLVSGWSRGKLYAVDFWDTGTNNNGPVLSRFVKK 60
Db 34 EHNPFVWHGIGGASNFAGIKSYLVSGWSRGKLYAVDFWDTGTNNNGPVLSRFVKK 93
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDDGKNKVENVTTLGGTNRSTTSKALPCTDPNQ 120
Db 94 VLDKTKGAKVDIVAHSMGGANTLYYIKNLDDGKKNVTVTGGANGLVSSRALPGTDPNQ 153
QY 121 KILYTSVSSADMVNVYLSKLDGAKVQIHGVGHIGLMMNSQVNSLIKEGLNGGLNTN 180
Db 154 KILYTSVSSADLIYVNSLSLIGARNLIHGVGHIGLTSQVKGKYLKEGLNGGGQNTN 213

RESULT 2

US-08-034-650-10
; Sequence 10, Application US/08034650
; Patent No. 5641671
; GENERAL INFORMATION:
; APPLICANT: BOS, Jannetje W.
; APPLICANT: FRENKEN, Leon G.
; APPLICANT: VERRIJS, Cornelis T.
; APPLICANT: VISSER, Christiaan
; TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
; TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/034,650
; APPLICATION NUMBER: US 07/727,235
; FILING DATE: 03-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PNK/5970/91731
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-034-650-10

Query Match 13.8%; Score 129.5; DB 1; Length 358;
Best Local Similarity 34.8%; Pred. No. 9.7e-06;
Matches 40; Conservative 16; Mismatches 42; Indels 17; Gaps 6;

QY 4 PVTVMHIGGASNF-----GIKSYLVSGWSRGKLYAVD---FWDKTTGTNNNGPV 53
Db 49 PVLVHGLAGTD-KFANVVDYWGIDSLQSHG---AKVIVANLSGFQSDGPN-GRGEQ 103

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VIRGINIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 22040
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,589A
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4336P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-589A-2

Query Match 12.5%; Score 117.5; DB 3; Length 363;
Best Local Similarity 29.8%; Pred. No. 0.0002;
Matches 39; Conservative 21; Mismatches 46; Indels 25; Gaps 8;
QY 4 PVMVHGIGGASFNAGIKSYLVSGWSR-----GKLYAVD---FWDKTGTNYNG 51
DB 54 PIILVHGLTGTD-KYGVVEY-----WYRIPEDLRAHGAAYVAVNLSGFQSDGPN-GRG 106
QY 52 PVLRSFVKVLDGTGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVVTLG-----GTNRS 107
DB 107 EQLLAFVKQVLAATGAQKNLIGHSGGL-TSRYVASV-APELVASVTTISTPHWGSQFA 164
QY 108 TTSKALPGTDP 118
DB 165 DFVQQLQTD 175

RESULT 5
US-09-336-601-1
; Sequence 1, Application US/09336601
; Patent No. 6184008
; GENERAL INFORMATION:
; APPLICANT: OHTA, Hiromichi
; APPLICANT: SUGAI, Takeshi
; APPLICANT: ISHII, Takeshi
; APPLICANT: MITSUDA, Satoshi
; TITLE OF INVENTION: PRODUCTION OF OPTICALLY ACTIVE SPHINGOID COMPOUND
; FILE REFERENCE: 2185-349P
; CURRENT APPLICATION NUMBER: US/09/336,601
; EARLIER FILING DATE: 1999-06-21
; EARLIER APPLICATION NUMBER: 09/034,007
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 363
; TYPE: PRT
; ORGANISM: E. coli JM 109/pAL 612 strain
US-09-336-601-1

Query Match 12.5%; Score 117.5; DB 3; Length 363;

Best Local Similarity 29.8%; Pred. No. 0.0002;
Matches 39; Conservative 21; Mismatches 46; Indels 25; Gaps 8;
QY 4 PVMVHGIGGASFNAGIKSYLVSGWSR-----GKLYAVD---FWDKTGTNYNG 51
DB 54 PIILVHGLTGTD-KYGVVEY-----WYRIPEDLRAHGAAYVAVNLSGFQSDGPN-GRG 106
QY 52 PVLRSFVKVLDGTGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVVTLG-----GTNRS 107
DB 107 EQLLAFVKQVLAATGAQKNLIGHSGGL-TSRYVASV-APELVASVTTISTPHWGSQFA 164
QY 108 TTSKALPGTDP 118
DB 165 DFVQQLQTD 175

RESULT 6
US-09-219-120-2
; Sequence 2, Application US/09219120
; Patent No. 6472189
; GENERAL INFORMATION:
; APPLICANT: TAKESHI, Ishii
; APPLICANT: SATOSHI, Mitsuda
; TITLE OF INVENTION: ESTERASE GENE AND ITS USE
; FILE REFERENCE: 20-4336P
; CURRENT APPLICATION NUMBER: US/09/219,120
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-09-219-120-2

Query Match 12.5%; Score 117.5; DB 4; Length 363;
Best Local Similarity 29.8%; Pred. No. 0.0002;
Matches 39; Conservative 21; Mismatches 46; Indels 25; Gaps 8;
QY 4 PVMVHGIGGASFNAGIKSYLVSGWSR-----GKLYAVD---FWDKTGTNYNG 51
DB 54 PIILVHGLTGTD-KYGVVEY-----WYRIPEDLRAHGAAYVAVNLSGFQSDGPN-GRG 106
QY 52 PVLRSFVKVLDGTGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVVTLG-----GTNRS 107
DB 107 EQLLAFVKQVLAATGAQKNLIGHSGGL-TSRYVASV-APELVASVTTISTPHWGSQFA 164
QY 108 TTSKALPGTDP 118
DB 165 DFVQQLQTD 175

RESULT 7
US-09-543-681A-7771
; Sequence 7771, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7771
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7771

Query Match 11.8%; Score 110.5; DB 4; Length 296;

Best Local Similarity 31.6%; Pred. No. 0.00085;
Matches 36; Conservative 15; Mismatches 44; Indels 19; Gaps 5;
QY 4 PVMVHGIGGASFN-----PAGIKSYLVSGWS--RGKLYAVDFWDXCTGTTNNNGPVL 54
DB 15 PIVLVHGLAG--FNEIVGFPEYGIADALRQDHQVFTASISAFN-----SNEVRGKQL 66
QY 55 SFVFKVLDLDEGAKKVDIVAHSMGGANTLYIKNLDDGKNKVENVVTLGTTNRST 108
DB 67 WQFVOTLQETQAKKNVIGHGQGLACRYVAANYP--DSVASVTISINGVNHGS 118

RESULT 8
US-08-400-422-3
; Sequence 3, Application US/08400422
; Patent No. 5681715
; GENERAL INFORMATION:
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Diderichsen, Boerge Krag
; APPLICANT: Buckley, Catherine M.
; APPLICANT: Hobson, Audrey
; APPLICANT: McConnell, David J.
; TITLE OF INVENTION: A process for the preparation of an active
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56817150 No. 5681715disk of No. 5681715th America, Inc.
; STREET: 405 Lexington Avenue, 62nd floor
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,422
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,763
; FILING DATE: 25-MAR-1993
; APPLICATION NUMBER: PCT/DK91/00402
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK92/00391
; FILING DATE: 18-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3663.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas cepacia
; STRAIN: DSM 3401
US-08-400-422-3

Query Match 11.8%; Score 110.5; DB 1; Length 364;
Best Local Similarity 31.0%; Pred. No. 0.0011;

Matches 35; Conservative 16; Mismatches 45; Indels 17; Gaps 6;
QY 4 PVMVHGIGGASFNAGIKSY-----LVSGWSRGKLYAVD---FWDKCTGTYNNGPVL 53
DB 54 PIVLVHGLTGT-D-KAGVLEWYWGQEDLQQEG---ATVIVANLSGFQDDGPN-GRGEQ 108
QY 54 LGRFVKVLDLDEGAKKVDIVAHSMGGANTLYIKNLDDGKNKVENVVTLGTTNR 106
DB 109 LLAYVKTVAATGATKCNLVGHKQGLTSRYVA--AVAPDLVASVTITGTPHR 159
RESULT 9
US-09-252-991A-27337
; Sequence 27337, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27337
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27337

Query Match 11.7%; Score 110; DB 4; Length 351;
Best Local Similarity 25.3%; Pred. No. 0.0012;
Matches 42; Conservative 30; Mismatches 54; Indels 40; Gaps 7;
QY 4 PVMVHGIGGASFNAGIKSYLVSGWSRGKLYAVDFW-----DKTG----- 45
DB 75 PIVLVHGLFG--FKSVG-----PVDYWHAIVPALEKDGAKVFATSQSPV 116
QY 46 -TNYNNGPVLRSFVKVLDLDEGAKKVDIVAHSMGGANTLYIKNLDDGKNKVENVVTLGTT 104
DB 117 NSNEVRGEQLLAQVEEVLTALTAETKLVCHSGQGM-IVRYVAGV-APOLVASVTITGTP 174
QY 105 NRST-TSKALPCTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQ 149
DB 175 HKGTPVADAVTGSEFLGPIGTEVIASAVEALFSVVDIVDGEWVK 220

RESULT 10
US-09-489-039A-7418
; Sequence 7418, Application US/09489039A
; Patent No. 6610838
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7418
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7418

Query Match 11.4%; Score 107.5; DB 4; Length 318;
Best Local Similarity 26.9%; Pred. No. 0.002;
Matches 46; Conservative 30; Mismatches 64; Indels 31; Gaps 8;

QY 5 VVMVHGIG-GAS--ENFAGIKSYLVSGWSRGLYAVDFWKTGTNNNG--PVLSEFV 58
 Db 68 VVLRSGGFCATGWANFSNDPLVEAGY-RVLLDDCGWGRKSDAIVNSGRSDINARIL 126
 QY 59 KXVLDEGAKVDIVAHSMGGANTLYYIKNLDGKNKVENVTLCG-----TNR 106
 Db 127 KSVVDQLGIDIKVHLLGNSGHSVAVAF-TLSWPBRVAKVLVGGGTGMSLFTPMPTG 184
 QY 107 STTSKAL---PGTDPNQKILYTSIYSSADMI-----VMNYLSKLDGAKN 147
 Db 185 IKLNLALYREPTIENLKQMSIFVETDRLDTALFEALNNWLRDRDLN 235

RESULT 11

US-09-134-001C-4568
 ; Sequence 4568, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 4568
 ; LENGTH: 690
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4568

Query Match 10.4%; Score 97.5; DB 4; Length 690;
 Best Local Similarity 22.5%; Pred. No. 0.075;
 Matches 50; Conservative 25; Mismatches 60; Indels 87; Gaps 10;
 QY 4 PVVMVHGIGGASFNFAGIKSYLVSGWSRGLYAVD-----FWDKTGT 46
 Db 310 PVVVFHGLG-----FAGDNQFSLAKPYWGTGTYNDRLTNEGYNVHEANIGAF---SS 361
 QY 47 NYNNGPVLSEFVKVLDGTGA-----FKVDIVAHSMGGAN 81
 Db 362 NYDRAVELYVYVKGGRVDYGAHAARYGRTYKGMRDWEPFKKHIFIGHSMGGQT 421
 QY 82 TLV---YIKN-----LDGG--NKVENVTLCGTNRSTTSKALPGTD 117
 Db 422 IRQWSEFLANGQEEIEYORHGGTISDLFTGGKDNVYASITTLTGPHTGTPADKIGT- 480
 QY 118 PNQKILYTSIYSSADMIVMNYLSKLDGAKNVQIH-GVGHIGL 158
 Db 481 --RKLVKETI-----NRIGLSGGKVDIDILGFSQWGL 511

RESULT 12

US-09-134-001C-4054
 ; Sequence 4054, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4054
 ; LENGTH: 699
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4054

Query Match 10.2%; Score 95.5; DB 4; Length 699;
 Best Local Similarity 22.7%; Pred. No. 0.13;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

QY 3 NPVVMVHGIGGASFNFAGIKSYLVSGWSRGLYAVDFWKTGTNNNGPVLSEFVKVL 62
 Db 338 NPSLVTHYWGDKDN---IRODLENGYEAYEASISAF-----GSNYDRAVELYIYIKGR 390
 QY 63 DETGA-----KKVDIVAHSMGGANTLYYIKNL----- 89
 Db 391 VDYGAHAARYGRTYKGMRDWEPFKKHIFIGHSMGG-QTIRQLELLRHGNPEE 449
 QY 90 -----DGG--NKVENVTLCGTNRSTTSKALPGTDPNQKILYTSIYSSAD 132
 Db 450 VEYQKHGEISPLFQGGHDMNVSSITTLTGPHTGTHASDLLG---NEAIVRLAYD--- 503
 QY 133 MIWMNYLSKLDGAKNVQI-HGVGHIGL 158
 Db 504 -----VGKMYGNKDSRVDPLGHEHGL 524

RESULT 13

US-09-584-568C-6
 ; Sequence 6, Application US/09584568C
 ; Patent No. 6500657
 ; GENERAL INFORMATION:
 ; APPLICANT: Glucksmann, Maria, Alexandra et al.
 ; TITLE OF INVENTION: 33167, A NOVEL HUMAN HYDROLASE AND USES THEREFOR
 ; FILE REFERENCE: MNI-140
 ; CURRENT APPLICATION NUMBER: US/09/584,568C
 ; CURRENT FILING DATE: 2000-05-31
 ; PRIOR APPLICATION NUMBER: 60/193,954
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 299
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-09-584-568C-6

Query Match 10.1%; Score 94.5; DB 4; Length 299;
 Best Local Similarity 24.5%; Pred. No. 0.047;
 Matches 27; Conservative 24; Mismatches 40; Indels 19; Gaps 3;
 QY 2 HNPVVMVHGIGGASFNFAGIKSYLVSGWSRGLYAVDFWKTGTNNNGP----- 52
 Db 45 NSPLVIVHGLFGQKQNNVSGKALHKK--LEAPYAVDV-----RNHGSFHTETWTSYE 97
 QY 53 ---VLSRFVKVLDGTGAKVDIVAHSMGGANTLYYIKNLDGKNKVENV 99
 Db 98 MAEDJVLFDKVKETTKKTRVNLIGHSMGGKIVMRLAIDSKWSDRIEKLI 147

RESULT 14

US-09-134-001C-3301
 ; Sequence 3301, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR FILING DATE: 1997-11-08
 ; NUMBER OF SEQ ID NOS: 5674

```
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3301
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3301

Query Match      10.0%; Score 93.5; DB 4; Length 292;
Best Local Similarity 21.8%; Pred. No. 0.058;
Matches 43; Conservative 26; Mismatches 47; Indels 81; Gaps 8;

QY 6 VVHVGIGGASFAGIKSYLVSQW-----SEGKLY-----A 37
Db 52 LFLHGYGGSERS-----ETFMVKQALNKNVINEVITARVSSEKVFYFDKLSSEDAANPIVK 107
QY 38 VDFWD-KTGTNYNGPVLRSFKKVLDETGAKKYDIVAHSMGGANTLYIKNLDDGKNKE 96
Db 108 VEFKDKTGNFKENAYWIKVELSKSQFG:QQNFVGHSMGNISFAFYMKNY----- 160
QY 97 NVVTLGGTNRSTTSKALPGTDPNOKILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHI 156
Db 161 -----GDD-----RHLPL--KKEVNIAGVING 181
QY 157 GLLMNSQVNSLI--KEG 171
Db 182 ILMNENVEIIVDKQG 198
```

```
RESULT 15
US-09-584-568C-8
; Sequence 8, Application US/09584568C
; Patent No. 6500657
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria, Alexandra et al.
; TITLE OF INVENTION: 33167, A NOVEL HUMAN HYDROLASE AND USES THEREFOR
; FILE REFERENCE: MN1-140
; CURRENT APPLICATION NUMBER: US/09/584,568C
; CURRENT FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/193,954
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-584-568C-8
```

```
Query Match      9.9%; Score 92.5; DB 4; Length 308;
Best Local Similarity 26.4%; Pred. No. 0.08;
Matches 23; Conservative 23; Mismatches 36; Indels 5; Gaps 3;

QY 4 PVVNVHIGGASFAGIKSYLVSQWSRGKLYAVD---FWDXTGTNYNGPVLRSFVKK 60
Db 54 PLLTYHGLFGSKQNRGISKALVRK-VSR-KYVAIDVRNHGSPHSSVHNSKANSDELRL 111
QY 61 VLDETGAKKYDIVAHSMGGANTLYIYIK 87
Db 112 FMEQRSHFNAACMCHSMGGRSMYFAR 138
```

Search completed: April 23, 2004, 10:14:40
Job time : 16.1531 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 23, 2004, 10:01:12 ; Search time 46.3776 Seconds
(without alignments)
1096.620 Million cell updates/sec

Title: US-09-905-666A-75
Perfect score: 939
Sequence: 1 EBNPVVHVGIGGASFNFAG.....NSQVNSLIKEGLNGGLNTN 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_29Jan04:*
- 1: Geneseq1380s:*
 - 2: Geneseq1990s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001s:*
 - 5: Geneseq2002s:*
 - 6: Geneseq2003as:*
 - 7: Geneseq2003bs:*
 - 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	939	100.0	180	5	Aau83861 Bacillus
2	927	98.7	180	5	Aau83890 Bacillus
3	925	98.5	180	5	Aau83864 Bacillus
4	924	98.4	180	5	Aau83884 Bacillus
5	923	98.3	180	5	Aau83862 Bacillus
6	923	98.3	180	5	Aau83894 Bacillus
7	922	98.2	180	5	Aau83873 Bacillus
8	920	98.0	180	5	Aau83863 Bacillus
9	920	98.0	212	5	Aau83845 Bacillus
10	920	98.0	212	5	Aau83844 Bacillus
11	919	97.9	180	5	Aau83885 Bacillus
12	917	97.7	180	5	Aau83868 Bacillus
13	917	97.7	180	5	Aau83893 Bacillus
14	914	97.3	180	5	Aau83888 Bacillus
15	913	97.2	180	5	Aau83889 Bacillus
16	913	97.2	180	5	Aau83891 Bacillus
17	913	97.2	212	5	Aau83848 Bacillus
18	912	97.1	180	5	Aau83867 Bacillus
19	911	97.0	180	5	Aau83887 Bacillus
20	911	97.0	180	5	Aau83886 Bacillus
21	909	96.8	212	5	Aau83847 Bacillus
22	909	96.8	212	5	Aau83841 Bacillus
23	907	96.6	180	5	Aau83883 Bacillus
24	906	96.5	180	5	Aau83874 Bacillus
25	906	96.5	180	5	Aau83872 Bacillus

26	906	96.5	212	5	Aau83846 Bacillus
27	905	96.4	180	5	Aau83880 Bacillus
28	904	96.3	180	5	Aau83892 Bacillus
29	902	96.1	180	5	Aau83870 Bacillus
30	902	96.1	180	5	Aau83866 Bacillus
31	901	96.0	180	5	Aau83871 Bacillus
32	897	95.5	180	5	Aau83869 Bacillus
33	895	95.3	180	5	Aau83882 Bacillus
34	891	94.9	180	5	Aau83875 Bacillus
35	889	94.7	180	5	Aau83881 Bacillus
36	887	94.5	180	5	Aau83876 Bacillus
37	887	94.5	180	5	Aau83879 Bacillus
38	886	94.4	212	5	Aau83855 Bacillus
39	882	93.9	212	5	Aau83849 Bacillus
40	881	93.8	180	5	Aau83877 Bacillus
41	881	93.8	212	5	Aau83842 Bacillus
42	880	93.7	180	5	Aau83878 Bacillus
43	872	92.9	212	5	Aau83856 Bacillus
44	869	92.5	212	5	Aau83854 Bacillus
45	862	91.8	212	5	Aau83843 Bacillus

ALIGNMENTS

RESULT 1
AAU83861
ID AAU83861 standard; protein; 180 AA.
XX
AC AAU83861;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #21.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.
XX
OS Synthetic.
XX
PN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US022160.
XX
PR 13-JUL-2000; 2000US-0217954P.
XX
PA 21-JUN-2001; 2001US-0300378P.
XX
PA (MAXY-) MAXYGEN INC.
XX
Giver LJ, Minshull J, Vogel K;
WPI; 2002-171805/22.
N-PSDB; ABK33839.
XX
Nucleic acids encoding lipase enzymes which are useful as supplements in
animal feeds, as agents of flavor modification and for treating Crohn's
disease and celiac disease.
PS
Claim 5; Page 141; 196pp; English.
XX
The invention relates to new Bacillus lipase enzymes and the nucleic
acids encoding them. The lipase polypeptides are useful as supplements in
animal feeds, as agents of flavour modification and fat modification in
human foodstuffs (e.g. cheese), as agents in the creation of food
emulsifiers, as agents for tanning/processing of leather and as cleaning
agents. They are also useful for treating Crohn's disease, cystic
fibrosis, coeliac disease, indigestion, obesity and other

CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
XX
SQ Sequence 180 AA;
Query Match 100.0%; Score 939; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 6,5e-87; Indels 0; Gaps 0;
Matches 180; Conservative 0; Mismatches 0;
QY 1 EHNPMVVMHGIIGGASFNAGIKSYLVSQWGRGKLYAVDFWDKGTGTNNNGPVLRSFVKK 60
DB 1 EHNPMVVMHGIIGGASFNAGIKSYLVSQWGRGKLYAVDFWDKGTGTNNNGPVLRSFVKK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDDGKNVENVTLLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDDGKNVENVTLLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIWMVYLSKLDGAKNQVHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
DB 121 KILYTSIYSSADMIWMVYLSKLDGAKNQVHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
RESULT 2
AAU83890
ID AAU83890 standard; protein; 180 AA.
XX
XX
AC AAU83890;
XX
XX
DT 08-MAY-2002 (first entry)
XX
XX
DE Bacillus lipase polypeptide #50.
XX
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW Gastrointestinal.
XX
XX
OS Synthetic.
XX
XX
FN WO200206457-A2.
XX
XX
PD 24-JAN-2002.
XX
XX
PF 13-JUL-2001; 2001WO-US022160.
XX
XX
PR 13-JUL-2000; 2000US-0217954P.
PR 21-JUN-2001; 2001US-0300378P.
XX
XX
PA (MAXY-) MAXYGEN INC.
XX
XX
PI Giver LJ, Minshull J, Vogel K;
XX
XX
DR WPI; 2002-171805/22.
DR N-PSDB; ABK33883.
XX
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements in
PT animal feeds, as agents of flavor modification and for treating Crohn's
PT disease and celiac disease.
XX
XX
PS Claim 5; Page 145; 196pp; English.
XX
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic

CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
XX
SQ Sequence 180 AA;
Query Match 98.7%; Score 927; DB 5; Length 180;
Best Local Similarity 98.3%; Pred. No. 1.1e-85;
Matches 177; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 EHNPMVVMHGIIGGASFNAGIKSYLVSQWGRGKLYAVDFWDKGTGTNNNGPVLRSFVKK 60
DB 1 EHNPMVVMHGIIGGASFNAGIKSYLVSQWGRGKLYAVDFWDKGTGTNNNGPVLRSFVKK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDDGKNVENVTLLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLDDGKNVENVTLLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIWMVYLSKLDGAKNQVHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
DB 121 KILYTSIYSSADMIWMVYLSKLDGAKNQVHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
RESULT 3
AAU83864
ID AAU83864 standard; protein; 180 AA.
XX
XX
AC AAU83864;
XX
XX
DT 08-MAY-2002 (first entry)
XX
XX
DE Bacillus lipase polypeptide #24.
XX
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW Gastrointestinal.
XX
XX
OS Synthetic.
XX
XX
FN WO200206457-A2.
XX
XX
PD 24-JAN-2002.
XX
XX
PF 13-JUL-2001; 2001WO-US022160.
XX
XX
PR 13-JUL-2000; 2000US-0217954P.
PR 21-JUN-2001; 2001US-0300378P.
XX
XX
PA (MAXY-) MAXYGEN INC.
XX
XX
PI Giver LJ, Minshull J, Vogel K;
XX
XX
DR WPI; 2002-171805/22.
DR N-PSDB; ABK33842.
XX
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements in
PT animal feeds, as agents of flavor modification and for treating Crohn's
PT disease and celiac disease.
XX
XX
PS Claim 5; Page 141-142; 196pp; English.
XX
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning

CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 XX Sequence 180 AA;

Query Match 98.5%; Score 925; DB 5; Length 180;
 Best Local Similarity 97.8%; Pred. No. 1.7e-85;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EHNPMVVMHVGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTNTYNNNGPVLSEFVKK 60
 DB 1 EHNPMVVMHVGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTNTYNNNGPVLSEFVKK 60
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVTLLGGTNRSTTSKALPGTDPNQ 120
 DB 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVTLLGGTNRSTTSKALPGTDPNQ 120
 QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
 DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180

RESULT 4
 AAU83884
 ID AAU83884 standard; protein; 180 AA.
 AC AAU83884;
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #44.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 OS Synthetic.
 XX
 XX WO200206457-A2.
 XX
 XX 24-JAN-2002.
 XX
 XX 13-JUL-2001; 2001WO-US022160.
 XX
 XX 13-JUL-2000; 2000US-0217954P.
 XX 21-JUN-2001; 2001US-0300378P.
 XX (MAXY-) MAXYGEN INC.
 XX
 XX Giver LJ, Minshull J, Vogel K;
 XX
 XX WPI; 2002-171805/22.
 XX N-PSDB; ABK3862.
 XX
 XX Nucleic acids encoding lipase enzymes which are useful as supplements in
 XX animal feeds, as agents of flavor modification and for treating Crohn's
 XX disease and coeliac disease.
 XX
 XX Claim 5; Page 144; 196pp; English.

CC The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food

CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 XX Sequence 180 AA;

Query Match 98.4%; Score 924; DB 5; Length 180;
 Best Local Similarity 97.8%; Pred. No. 2.2e-85;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EHNPMVVMHVGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTNTYNNNGPVLSEFVKK 60
 DB 1 EHNPMVVMHVGIGGASFNAGIKSYLVSGWSRGKLYAVDFWDTGTNTYNNNGPVLSEFVKK 60
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVTLLGGTNRSTTSKALPGTDPNQ 120
 DB 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNVENVTLLGGTNRSTTSKALPGTDPNQ 120
 QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180
 DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 180

RESULT 5
 AAU83862
 ID AAU83862 standard; protein; 180 AA.
 AC AAU83862;
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #22.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 OS Synthetic.
 XX
 XX WO200206457-A2.
 XX
 XX 24-JAN-2002.
 XX
 XX 13-JUL-2001; 2001WO-US022160.
 XX
 XX 13-JUL-2000; 2000US-0217954P.
 XX 21-JUN-2001; 2001US-0300378P.
 XX (MAXY-) MAXYGEN INC.
 XX
 XX Giver LJ, Minshull J, Vogel K;
 XX
 XX WPI; 2002-171805/22.
 XX N-PSDB; ABK3840.
 XX
 XX Nucleic acids encoding lipase enzymes which are useful as supplements in
 XX animal feeds, as agents of flavor modification and for treating Crohn's
 XX disease and coeliac disease.
 XX
 XX Claim 5; Page 141; 196pp; English.

CC The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in

CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 SQ Sequence 180 AA;

Query Match 98.3%; Score 923; DB 5; Length 180;
 Best Local Similarity 97.8%; Pred. No. 2.7e-85;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EHNPPVVMVHGIGGASFNPAIGIKSYLVSQWMSRGKLYAVDFWDKTGTNTNNGPVLRSFVKX 60
 DB 1 EHNPPVVMVHGIGGASFNPAIGIKSYLVSQWMSRGKLYAVDFWDKTGTNTNNGPVLRSFVKD 60
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
 DB 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLLGGANRSTTSKALPGTDPNQ 120
 QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLMMNSQVNSLIKEGLNGGLNTN 180
 DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLMMNSQVNSLIKEGLNGGLNTN 180

RESULT 6
 AAU83894
 ID AAU83894 standard; protein; 180 AA.
 AC AAU83894;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #54.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 XX
 OS Synthetic.
 XX
 PN WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US022160.
 XX
 PR 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 XX Giver LJ, Minshull J, Vogel K;
 XX
 XX WPI; 2002-171805/22.
 DR N-PSDB; ABK33872.
 DR
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and coeliac disease.
 XX
 PS Claim 5; Page 145-146; 196pp; English.
 XX
 CC The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in

CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 SQ Sequence 180 AA;

Query Match 98.3%; Score 923; DB 5; Length 180;
 Best Local Similarity 97.8%; Pred. No. 2.7e-85;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EHNPPVVMVHGIGGASFNPAIGIKSYLVSQWMSRGKLYAVDFWDKTGTNTNNGPVLRSFVKX 60
 DB 1 EHNPPVVMVHGIGGASFNPAIGIKSYLVSQWMSRGKLYAVDFWDKTGTNTNNGPVLRSFVKQ 60
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLLGGTNRSTTSKALPGTDPNQ 120
 DB 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVTLLGGANRSTTSKALPGTDPNQ 120
 QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLMMNSQVNSLIKEGLNGGLNTN 180
 DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLMMNSQVNSLIKEGLNGGLNTN 180

RESULT 7
 AAU83873
 ID AAU83873 standard; protein; 180 AA.
 AC AAU83873;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #33.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 XX
 OS Synthetic.
 XX
 PN WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US022160.
 XX
 PR 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 XX Giver LJ, Minshull J, Vogel K;
 XX
 XX WPI; 2002-171805/22.
 DR N-PSDB; ABK33851.
 DR
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and coeliac disease.
 XX
 PS Claim 5; Page 143; 196pp; English.
 XX
 CC The invention relates to new Bacillus lipase enzymes and the nucleic

CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
SQ Sequence 180 AA;

Query Match 98.2%; Score 922; DB 5; Length 180;
Best Local Similarity 97.2%; Pred. No. 3.5e-85;
Matches 175; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 EHNPPVVMVHGIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNNYNGPVLRSFVK 60
DB 1 EHNPPVVMVHGIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNNYNGPVLRSFVK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVTLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVTLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 8
AAU83863
ID AAU83863 standard; protein; 180 AA.
XX
AC AAU83863;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #23.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuffs; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.
XX
OS Synthetic.
XX
FN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US022160.
XX
FR 13-JUL-2000; 2000US-0217954P.
FR 21-JUN-2001; 2001US-0300378P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Giver LJ, Minshull J, Vogel K;
XX
DR WPI; 2002-171805/22.
DR N-PSDB; ABK3641.
XX
XX Nucleic acids encoding lipase enzymes which are useful as supplements in
PT animal feeds, as agents of flavor modification and for treating Crohn's
PT disease and celiac disease.
XX
PS Claim 5; Page 141; 196pp; English.

CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
SQ Sequence 180 AA;

Query Match 98.0%; Score 920; DB 5; Length 180;
Best Local Similarity 97.2%; Pred. No. 5.5e-85;
Matches 175; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 EHNPPVVMVHGIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNNYNGPVLRSFVK 60
DB 1 EHNPPVVMVHGIGGASFNFAKISYLSQGSRGKLYAVDFWDTGTNNYNGPVLRSFVK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVTLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLDGKNKVENVTLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180

RESULT 9
AAU83845
ID AAU83845 standard; protein; 212 AA.
XX
AC AAU83845;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #5.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuffs; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.
XX
OS Bacillus circulans.
XX
FN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US022160.
XX
FR 13-JUL-2000; 2000US-0217954P.
FR 21-JUN-2001; 2001US-0300378P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Giver LJ, Minshull J, Vogel K;
XX
DR WPI; 2002-171805/22.
DR N-PSDB; ABK3823.
XX
XX Nucleic acids encoding lipase enzymes which are useful as supplements in
PT animal feeds, as agents of flavor modification and for treating Crohn's
PT disease and celiac disease.
XX
PS Claim 20; Page 139; 196pp; English.

XX The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 SQ Sequence 212 AA;

Query Match 98.0%; Score 920; DB 5; Length 212;
 Best Local Similarity 97.2%; Pred. No. 6.9e-85;
 Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDKGTGNNYNGPVLRSFVKK 60
 Db 33 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDKGTGNNYNGPVLRSFVKK 92

Qy 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVVTGGTNRSTTSKALPGTDPNQ 120
 Db 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVVTGGTNRSTTSKALPGTDPNQ 152

Qy 121 KILYTSYSSADMIVMNYLSKLDGAKVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
 Db 153 KILYTSYSSADMIVMNYLSKLDGAKVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 212

RESULT 10

AAU83844
 ID AAU83844 standard; protein; 212 AA.
 XX
 AC AAU83844;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #4.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; anti-inflammatory; respiratory;
 KW gastrointestinal.
 XX
 OS Bacillus lentus.
 XX
 PN WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US022160.
 XX
 PR 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Giver LJ, Minshull J, Vogel K;
 XX
 DR N-PSDB; ABK33822.
 DR
 XX Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and celiac disease.
 PT

PS Claim 20; Page 138-139; 196pp; English.

XX The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX
 SQ Sequence 212 AA;

Query Match 98.0%; Score 920; DB 5; Length 212;
 Best Local Similarity 97.2%; Pred. No. 6.9e-85;
 Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDKGTGNNYNGPVLRSFVKK 60
 Db 33 EHNPMVVMHVGIGGASFNAGIKSVLSQGSRGKLYAVDFWDKGTGNNYNGPVLRSFVKK 92

Qy 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVVTGGTNRSTTSKALPGTDPNQ 120
 Db 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGKNKVENVVTGGTNRSTTSKALPGTDPNQ 152

Qy 121 KILYTSYSSADMIVMNYLSKLDGAKVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
 Db 153 KILYTSYSSADMIVMNYLSKLDGAKVQIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 212

RESULT 11

AAU83885
 ID AAU83885 standard; protein; 180 AA.
 XX
 AC AAU83885;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #45.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; anti-inflammatory; respiratory;
 KW gastrointestinal.
 XX
 OS Synthetic.
 XX
 PN WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US022160.
 XX
 PR 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Giver LJ, Minshull J, Vogel K;
 XX
 DR WPI; 2002-171805/22.
 DR N-PSDB; ABK33863.
 DR
 XX Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and celiac disease.
 PT

XX Claim 5; Page 144; 196pp; English.
 XX The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX Sequence 180 AA;
 SQ

Query Match 97.9%; Score 919; DB 5; Length 180;
 Best Local Similarity 97.2%; Pred. No. 7e-85; 2; Indels 0; Gaps 0;
 Matches 175; Conservative 3; Mismatches 2;

QY 1 EHNPMVVMHVGIGGASFNFAGIKSVLVSGWSRGKLYAVDFWDTGTNNNGPVLRSFVKK 60
 DB 1 EHNPMVVMHVGIGGASFNFAGIKSVLVSGWSRGKLYAVDFWDRGTNNNGPVLRSFVKK 60
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLGGKNKVENVTILGGTNRSTTSKALPGTDPNQ 120
 DB 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLGGKNKIENVTILGGANRSTTSKALPGTDPNQ 120
 QY 121 KILYTSIYSSADMIWMVYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGGLNTN 180
 DB 121 KILYTSIYSSADMIWMVYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGGLNTN 180

RESULT 12
 AAU83868
 ID AAU83868 standard; protein; 180 AA.
 XX
 AC AAU83868;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #28.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 XX
 OS Synthetic.
 XX
 PN WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US022160.
 XX
 PR 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Giver LJ, Minshull J, Vogel K;
 XX
 DR WPI; 2002-171805/22.
 DR N-PSDB; ABK3846.
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements in
 animal feeds, as agents of flavor modification and for treating Crohn's

PT disease and coeliac disease.
 XX Claim 7; Page 142; 196pp; English.
 XX The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention
 XX Sequence 180 AA;
 SQ

Query Match 97.7%; Score 917; DB 5; Length 180;
 Best Local Similarity 96.7%; Pred. No. 1.1e-84; 2; Indels 0; Gaps 0;
 Matches 174; Conservative 4; Mismatches 2;

QY 1 EHNPMVVMHVGIGGASFNFAGIKSVLVSGWSRGKLYAVDFWDTGTNNNGPVLRSFVKK 60
 DB 1 EHNPMVVMHVGIGGASFNFAGIKSVLVSGWSRGKLYAVDFWDTGTNNNGPVLRSFVKK 60
 QY 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLGGKNKVENVTILGGTNRSTTSKALPGTDPNQ 120
 DB 61 VLDETGAKKVDIVAHSMGGANTLYIYIKNLGGKNKIENVTILGGANRSTTSKALPGTDPNQ 120
 QY 121 KILYTSIYSSADMIWMVYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGGLNTN 180
 DB 121 KILYTSIYSSADMIWMVYLSKLDGAKNQIHGVGHIGLLMNSQVNSLIKEGLNGGGGLNTN 180

RESULT 13
 AAU83893
 ID AAU83893 standard; protein; 180 AA.
 XX
 AC AAU83893;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #53.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 XX
 OS Synthetic.
 XX
 PN WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US022160.
 XX
 PR 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Giver LJ, Minshull J, Vogel K;
 XX
 DR WPI; 2002-171805/22.
 DR N-PSDB; ABK38971.
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements in

PT animal feeds, as agents of flavor modification and for treating Crohn's
PT disease and coliac disease.
XX
XX Claim 5; Page 145; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
XX Sequence 180 AA;
SQ
Query Match 97.7%; Score 917; DB 5; Length 180;
Best Local Similarity 97.8%; Pred. No. 1.1e-84;
Matches 176; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EHNPFVVMVHGIGGASFNAGIKSYLVSGWSRGLYAVDFMDKTGTNNNGPVLRSFVKK 60
DB 1 EHNPFVVMVHGIGGASFNAGIKSYLVSGWSRDLKLYAVDFMDKTGTNNNGPVLRSFVK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLLGGNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLLGGNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVOIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVOIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 180
RESULT 14
AAU83888
ID AAU83888 standard; protein; 180 AA.
XX
XX AAU83888;
XX
XX 08-MAY-2002 (first entry)
XX
XX Bacillus lipase polypeptide #48.
XX
XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
XX human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
XX leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
XX coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
XX gastrointestinal lipid related condition; antiinflammatory; respiratory;
XX Gastrointestinal.
XX
XX Synthetic.
XX
XX WO200206457-A2.
XX
XX 24-JAN-2002.
XX
XX 13-JUL-2001; 2001WO-US022160.
XX
XX 13-JUL-2000; 2000US-0217954P.
XX
XX 21-JUN-2001; 2001US-0300378P.
XX
XX (MAXY-) MAXYGEN INC.
XX
XX Giver LJ, Minshull J, Vogel K;
XX
XX WPI; 2002-171805/22.
XX
XX N-PSDB; ABK33866.
XX

PT Nucleic acids encoding lipase enzymes which are useful as supplements in
PT animal feeds, as agents of flavor modification and for treating Crohn's
XX disease and coliac disease.
XX
XX Claim 5; Page 145; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
XX Sequence 180 AA;
SQ
Query Match 97.3%; Score 914; DB 5; Length 180;
Best Local Similarity 96.7%; Pred. No. 2.2e-84;
Matches 174; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EHNPFVVMVHGIGGASFNAGIKSYLVSGWSRGLYAVDFMDKTGTNNNGPVLRSFVKK 60
DB 1 EHNPFVVMVHGIGGASFNAGIKSYLVSGWSRDLKLYAVDFMDKTGTNNNGPVLRSFVKK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGNKVENVVTLLGGNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYYIKNLGGDKIENVVTLGGANRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMIVMNYLSKLDGAKNVOIHGVGHIGLLMNSQVNSLIKEGLNGGLNTN 180
DB 121 KILYTSIYSSADMIVMNYLSKLDGAKNVOIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 180
RESULT 15
AAU83889
ID AAU83889 standard; protein; 180 AA.
XX
XX AAU83889;
XX
XX 08-MAY-2002 (first entry)
XX
XX Bacillus lipase polypeptide #49.
XX
XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
XX human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
XX leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
XX coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
XX gastrointestinal lipid related condition; antiinflammatory; respiratory;
XX Gastrointestinal.
XX
XX Synthetic.
XX
XX WO200206457-A2.
XX
XX 24-JAN-2002.
XX
XX 13-JUL-2001; 2001WO-US022160.
XX
XX 13-JUL-2000; 2000US-0217954P.
XX
XX 21-JUN-2001; 2001US-0300378P.
XX
XX (MAXY-) MAXYGEN INC.
XX
XX Giver LJ, Minshull J, Vogel K;
XX
XX WPI; 2002-171805/22.
XX
XX N-PSDB; ABK33867.
XX

XX Nucleic acids encoding lipase enzymes which are useful as supplements in
PT animal feeds, as agents of flavor modification and for treating Crohn's
PT disease and celiac disease.
XX
PS Claim 5; Page 145; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, celiac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention
XX
SQ Sequence 180 AA;

Query Match 97.2%; Score 913; DB 5; Length 180;
Best Local Similarity 97.2%; Pred. No. 2.8e-84;
Matches 175; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 EHNPMVTHGIGGASFNFAGIKSYLVSGKSRGKLYAVDFWDKTGTNNNGPVLSPFVK 60
DB 1 EHNPMVTHGIGGASFNFAGIKSYLVSGKSRGKLYAVDFWDKTGTNNNGPVLSPFVK 60
QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLGDNKVENNVTLGGTNRSTTSKALPGTDPNQ 120
DB 61 VLDETGAKKVDIVAHSMGGANTLYIKNLGDNKVENNVTLGGTNRSTTSKALPGTDPNQ 120
QY 121 KILYTSIYSSADMVVMNYLSKLDGAKNVOIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 180
DB 121 KILYTSIYSSADMVVMNYLSKLDGAKNVOIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 180

Search completed: April 23, 2004, 10:11:56
Job time : 47.3776 secs